

=> d his nofile

(FILE 'HOME' ENTERED AT 09:54:26 ON 05 SEP 2006)

FILE 'CAPLUS' ENTERED AT 09:54:40 ON 05 SEP 2006

SET LINE 250

SET DETAIL OFF

E US1999-235416/AP,PRN 25

SET LINE LOGIN

SET DETAIL LOGIN

L1 1 SEA ABB=ON US99-235416/PRN  
D SCAN

L2 45 SEA ABB=ON SAKOWICZ R?/AU

L3 1091 SEA ABB=ON GOLDSTEIN L?/AU

L4 61 SEA ABB=ON (THERMOMYCES LANUGINOSUS/OBI OR TL/OBI) (W) GAMMA/OBI

E TEST KITS+ALL/CT

L5 17063 SEA ABB=ON TEST KITS/CT

L6 9 SEA ABB=ON (L2 AND L3) OR ((L2 OR L3) AND L4)

L7 1841 SEA ABB=ON KINESINS/CT

L8 2 SEA ABB=ON THERMOMYCES LANUGINOSUS/CT (L) GAMMA/OBI

L9 20619 SEA ABB=ON MICROTUBULE#/OBI

L10 3352 SEA ABB=ON MOTOR/OBI (L) PROTEIN#/OBI

FILE 'REGISTRY' ENTERED AT 09:59:03 ON 05 SEP 2006

E PROTEIN KINASE/CN

L11 1 SEA ABB=ON "PROTEIN KINASE"/CN

FILE 'REGISTRY' ENTERED AT 09:59:23 ON 05 SEP 2006

D IDE

FILE 'CAPLUS' ENTERED AT 09:59:35 ON 05 SEP 2006

L12 97768 SEA ABB=ON L11 OR PROTEIN KINASE#/OBI

L13 0 SEA ABB=ON L8 NOT L4

L14 1 SEA ABB=ON L4 AND (L5 OR L7 OR L9 OR L10 OR L12)

L15 220 SEA ABB=ON L7 AND L9 AND L10

L16 161 SEA ABB=ON L9 (L) L10 AND L7

L17 48 SEA ABB=ON END DIRECT?/OBI

L18 3 SEA ABB=ON L15 AND L17

E SCREENING/CT

L19 42502 SEA ABB=ON L12 (L) (MODULAT?/OBI OR INHIBIT?/OBI OR ACTIVAT?/OBI  
)

L20 11 SEA ABB=ON L15 AND L19

L21 0 SEA ABB=ON L16 AND L19

D QUE L20

D SCAN TI L20

L22 1 SEA ABB=ON MAP/TI AND L20  
D SCAN

L23 477 SEA ABB=ON L19 (L) ANST/RL

L24 3 SEA ABB=ON L15 AND L23

L25 233 SEA ABB=ON L19 AND L5

D SCA L1

L26 20 SEA ABB=ON L7 AND L25

D QUE

L27 8 SEA ABB=ON L7 AND L25 AND L23

D SCAN TI

FILE 'WPIX' ENTERED AT 10:38:16 ON 05 SEP 2006

L28 36 SEA ABB=ON SAKOWICZ R?/AU

L29 64 SEA ABB=ON GOLDSTEIN L?/AU

L30 1 SEA ABB=ON (THERMOMYCES LANUGINOSUS/BI,ABEX OR TL/BI,ABEX) (A)G  
AMMA/BI,ABEX  
D TRIAL

L31 3 SEA ABB=ON L28 AND L29  
D TRIAL 1-3

L32 252 SEA ABB=ON KINESIN#/BI,ABEX

L33 811 SEA ABB=ON MICROTUBULE#/BI,ABEX OR MICRO TUBULE#/BI,ABEX

L34 120 SEA ABB=ON MOTOR PROTEIN#/BI,ABEX

L35 1863 SEA ABB=ON END DIRECT?/BI,ABEX

L36 4006 SEA ABB=ON PROTEIN KINASE#/BI,ABEX

L37 105 SEA ABB=ON L32 AND (L33 OR L34 OR L35)

L38 54 SEA ABB=ON L32 AND L33 AND L34

L39 3 SEA ABB=ON L32 AND L33 AND L34 AND L35

L40 1 SEA ABB=ON L37 AND L36

L41 2492 SEA ABB=ON L36 (3A) (MODULAT?/BI,ABEX OR INHIBIT?/BI,ABEX OR  
ACTIVAT?/BI,ABEX)

L42 3 SEA ABB=ON L32 AND L41  
D TRIAL 1-3

L43 302435 SEA ABB=ON SCREEN?/BI,ABEX

L44 1372 SEA ABB=ON DRUG#/BI,ABEX (2A) CANDIDATE#/BI,ABEX

L45 484 SEA ABB=ON L41 AND (L43 OR L44)

L46 15 SEA ABB=ON L41 AND L43 AND L44  
D TRIAL 1-5  
D QUE

L47 45 SEA ABB=ON L41 AND (L33 OR L34 OR L35)

L48 9 SEA ABB=ON L41 AND (L33 OR L34 OR L35) AND (L43 OR L44)  
D TRIAL 1-3  
D TRIAL L31 1-3

FILE 'STNGUIDE' ENTERED AT 10:52:47 ON 05 SEP 2006

FILE 'WPIX' ENTERED AT 10:58:19 ON 05 SEP 2006

L49 11026 SEA ABB=ON L43 (2A) (DRUG#/BI,ABEX OR COMPOUND#/BI,ABEX)

L50 2 SEA ABB=ON L41 AND (L33 OR L34 OR L35) AND (L44 OR L49)  
D TRIAL 1-2  
D KWIC 1-2

L51 38 SEA ABB=ON L41 (S) ((L44 OR L49))

L52 19 SEA ABB=ON L41 (10A) ((L44 OR L49))

L53 15 SEA ABB=ON L41 (5A) ((L44 OR L49))

L54 0 SEA ABB=ON L51 AND (L33 OR L34 OR L35)

FILE 'STNGUIDE' ENTERED AT 11:01:44 ON 05 SEP 2006

FILE 'WPIX' ENTERED AT 11:02:37 ON 05 SEP 2006

L55 50839 SEA ABB=ON ASSAY#/BI,ABEX

L56 3543 SEA ABB=ON L43 (3A) L55

L57 26 SEA ABB=ON L56 AND (L49 OR L44) AND L41

L58 1 SEA ABB=ON L57 AND (L33 OR L34 OR L35)

L59 2 SEA ABB=ON L56 (S) (L49 OR L44) (S) L41

INDEX '1MOBILITY, 2MOBILITY, ABI-INFORM, ADISCTI, AEROSPACE, AGRICOLA,  
ALUMINIUM, ANABSTR, ANTE, APOLLIT, AQUALINE, AQUASCI, AQUIRE, BABS,  
BIBLIODATA, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA,  
CAOLD, CAPLUS, CASREACT, CBNB, CEABA-VTB, CERAB, ...' ENTERED AT 11:05:41  
ON 05 SEP 2006

SEA (THERMOMYCES LANUGINOSUS OR TL) (A) GAMMA

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8 FILE AEROSPACE  
1 FILE AGRICOLA  
11 FILE ANABSTR

1 FILE AQUASCI  
3 FILE BIOENG  
14 FILE BIOSIS  
2 FILE BIOTECHNO  
4 FILE CABA  
1 FILE CAOLD  
63 FILE CAPLUS  
1 FILE CIVILENG  
46 FILE COMPENDEX  
2 FILE COMPUSCIENCE  
1 FILE CONFSCI  
1 FILE DDFU  
7 FILE DGENE  
5 FILE DISSABS  
1 FILE DRUGU  
2 FILE EMBAL  
16 FILE EMBASE  
150 FILE ENERGY  
1 FILE ENVIROENG  
9 FILE EPFULL  
9 FILE ESBIOBASE  
2 FILE GBFULL  
2 FILE GENBANK  
1 FILE GEOREF  
3 FILE HEALSAFE  
6 FILE IFIPAT  
152 FILE INIS  
4 FILE INPADOC  
176 FILE INSPEC  
10 FILE INSPHYS  
1 FILE JAPIO  
16 FILE JICST-EPLUS  
3 FILE LIFESCI  
3 FILE MECHENG  
11 FILE MEDLINE  
6 FILE METADEX  
33 FILE NTIS  
21 FILE PASCAL  
9 FILE PATDPAFULL  
12 FILE PCTFULL  
5 FILE POLLUAB  
58 FILE SCISEARCH  
1 FILE SOLIDSTATE  
6 FILE TEMA  
21 FILE TOXCENTER  
1 FILE TULSA  
1 FILE ULIDAT  
19 FILE USPATFULL  
3 FILE USPAT2  
1 FILE WPIDS  
1 FILE WPINDEX

L60 QUE ABB=ON (THERMOMYCES LANUGINOSUS OR TL) (A) GAMMA

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FILE 'STNGUIDE' ENTERED AT 11:10:58 ON 05 SEP 2006

FILE 'DRUGU, JICST-EPLUS, AGRICOLA, PASCAL, CABA, BIOTECHNO, BIOSIS,  
ESBIOBASE, LIFESCI, CONFSCI, DISSABS, JAPIO, ANABSTR, SCISEARCH' ENTERED  
AT 11:15:21 ON 05 SEP 2006

L61 138 SEA ABB=ON SAKOWICZ R?/AU

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L62      4782 SEA ABB=ON  GOLDSTEIN L?/AU
L63      147 SEA ABB=ON  (THERMOMYCES LANUGINOSUS OR TL) (A) GAMMA
L64     13861 SEA ABB=ON  KINESIN#
L65     132140 SEA ABB=ON  MICROTUBULE# OR MICRO TUBULE#
L66      7756 SEA ABB=ON  MOTOR PROTEIN#
L67     2654 SEA ABB=ON  END DIRECT?
L68      40 SEA ABB=ON  (L61 AND L62) OR ((L61 OR L62) AND L63)
L69     22 DUP REM L68 (18 DUPLICATES REMOVED)
          ANSWERS '1-2' FROM FILE DRUGU
          ANSWER '3' FROM FILE PASCAL
          ANSWERS '4-5' FROM FILE BIOTECHNO
          ANSWERS '6-17' FROM FILE BIOSIS
          ANSWER '18' FROM FILE LIFESCI
          ANSWERS '19-20' FROM FILE CONFSCI
          ANSWERS '21-22' FROM FILE SCISEARCH
L70     567385 SEA ABB=ON  PROTEIN KINASE#
L71      3 SEA ABB=ON  L63 AND (L64 OR L65 OR L66 OR L67 OR L70)
L72     377 SEA ABB=ON  L64 AND L65 AND L66 AND L67
L73     83 SEA ABB=ON  L64 AND L65 (5A) L66 (5A) L67
L74     12 SEA ABB=ON  L64 (3A) L65 (3A) L66 (3A) L67
L75     20 SEA ABB=ON  L64 (5A) L65 (5A) L66 (5A) L67
L76     262577 SEA ABB=ON  L70 (3A) ((MODULAT? OR INHIBIT? OR ACTIVAT?))
L77     2376 SEA ABB=ON  (SCREEN? OR CANDIDATE#) (3A) (DRUG# OR COMPOUND#) (5A)
          ASSAY?
L78      0 SEA ABB=ON  L76 (S) L77 AND (L64 OR L65 OR L66 OR L67)
L79     12 SEA ABB=ON  L76 (S) L77

FILE 'MEDLINE' ENTERED AT 11:23:32 ON 05 SEP 2006
L80      13 SEA ABB=ON  SAKOWICZ R?/AU
L81     1168 SEA ABB=ON  GOLDSTEIN L?/AU
L82      11 SEA ABB=ON  (THERMOMYCES LANUGINOSUS OR TL) (A) GAMMA
L83      4 SEA ABB=ON  (L80 AND L81) OR ((L80 OR L81) AND L82)
          D TRIAL 1-4
          E KINESIN+ALL/CT
L84     2094 SEA ABB=ON  KINESIN/CT
          E MICROTUBULES+ALL/CT
L85     17967 SEA ABB=ON  MICROTUBULES/CT
L86     76212 SEA ABB=ON  ENZYME INHIBITORS/CT
          E MOTOR PROTEIN/CT
L87     1529 SEA ABB=ON  MOTOR PROTEIN#
L88     359 SEA ABB=ON  END DIRECT?
L89      0 SEA ABB=ON  L82 AND (L84 OR L85 OR L86 OR L87 OR L88)
          D TRIAL L82 1-3
          D TRIAL L82 4-11
L90     325 SEA ABB=ON  L84 AND L85 AND (L87 OR L88)
L91     34 SEA ABB=ON  L84 AND L85 AND L87 AND L88
L92      9 SEA ABB=ON  L87 (8A) L88 AND L84 AND L85
          E PROTEIN KINASE/CT
          E E3+ALL
L93     184405 SEA ABB=ON  PROTEIN KINASES+NT/CT
          E SCREENING/CT
          E E4+ALL
L94     22924 SEA ABB=ON  DRUG EVALUATION, PRECLINICAL/CT
L95     102 SEA ABB=ON  L93 AND L94 AND L86
L96     64 SEA ABB=ON  L93/MAJ AND L94 AND L86/MAJ
L97     13 SEA ABB=ON  L93/MAJ AND L94 (L) MT/CT AND L86/MAJ
          D TRIAL 1-4
L98     28397 SEA ABB=ON  L93 (L) AI/CT
L99     8557 SEA ABB=ON  L98/MAJ
L100    21967 SEA ABB=ON  ENZYME ACTIVATION/CT (L) DE/CT

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L101 189 SEA ABB=ON L100/MAJ  
 L102 19 SEA ABB=ON ((L93/MAJ AND L101) OR L99) AND L94(L)MT/CT  
 L103 4668 SEA ABB=ON L94(L)MT/CT  
 L104 1977 SEA ABB=ON L103/MAJ  
 L105 10 SEA ABB=ON ((L93/MAJ AND L101) OR L99) AND L104  
 D TRIAL 1-3  
 L106 0 SEA ABB=ON L95 AND L84

FILE 'EMBASE' ENTERED AT 11:33:37 ON 05 SEP 2006

L107 13 SEA ABB=ON SAKOWICZ R?/AU  
 L108 922 SEA ABB=ON GOLDSTEIN L?/AU  
 L109 16 SEA ABB=ON (THERMOMYCES LANUGINOSUS OR TL) (A) GAMMA  
 L110 5 SEA ABB=ON (L107 AND L108) OR ((L107 OR L108) AND L109)  
 D TRIAL 1-5

FILE 'STNGUIDE' ENTERED AT 11:34:20 ON 05 SEP 2006

FILE 'EMBASE' ENTERED AT 12:01:08 ON 05 SEP 2006

L111 5 SEA ABB=ON (L107 AND L108) OR ((L107 OR L108) AND L109)  
 D TRIAL 1-5  
 L112 2142 SEA ABB=ON KINESIN/CT  
 L113 3476 SEA ABB=ON MICROTUBULE ASSEMBLY/CT  
 L114 754 SEA ABB=ON MICROTUBULE PROTEIN/CT  
 L115 13611 SEA ABB=ON MICROTUBULE/CT  
 L116 316 SEA ABB=ON END DIRECT?  
 E MOTOR PROTEIN/CT  
 E E3+ALL  
 L117 569 SEA ABB=ON MOTOR PROTEIN/CT OR MOLECULAR MOTOR/CT  
 L118 0 SEA ABB=ON L109 AND (L112 OR L113 OR L114 OR L115 OR L116 OR  
 L117)  
 L119 7 SEA ABB=ON L112 AND (L113 OR L114 OR L115) AND L116 AND L117  
 E ENZYME ACTIVAT/CT  
 L120 68045 SEA ABB=ON ENZYME ACTIVATION/CT  
 L121 1083 SEA ABB=ON ENZYME ACTIVATOR/CT  
 E ENZYME MODULAT/CT  
 L122 39 SEA ABB=ON ENZYME MODULATION/CT  
 L123 16880 SEA ABB=ON ENZYME INHIBITOR/CT  
 L124 89209 SEA ABB=ON ENZYME INHIBITION/CT  
 E PROTEIN KINASE/CT  
 L125 20757 SEA ABB=ON PROTEIN KINASE+NT/CT  
 L126 2690 SEA ABB=ON L125/MAJ AND (L120 OR L121 OR L122 OR L123 OR  
 L124)  
 L127 31 SEA ABB=ON L126 AND (L112 OR L113 OR L114 OR L115 OR L116 OR  
 L117 OR L109)  
 L128 4 SEA ABB=ON GENERAL REVIEW/DT AND L127  
 D TRIAL 1-4  
 E ENZYME ACTIVITY/CT  
 L129 221084 SEA ABB=ON ENZYME ACTIVITY/CT  
 E DRUG SCREENING/CT  
 E E3+ALL  
 L130 74504 SEA ABB=ON DRUG SCREENING/CT  
 E E19+ALL  
 L131 22260 SEA ABB=ON SCREENING TEST/CT  
 L132 4100 SEA ABB=ON L125/MAJ AND (L120 OR L121 OR L122 OR L123 OR L124  
 OR L129)  
 L133 24 SEA ABB=ON L132 AND (L130 OR L131)  
 D TRIAL 1-4  
 L134 4072 SEA ABB=ON PROTEIN KINASE INHIBITOR/CT  
 L135 1431 SEA ABB=ON L134/MAJ  
 L136 53 SEA ABB=ON L135 AND (L130 OR L131)

L137 71 SEA ABB=ON L133 OR L136  
E ANALYTIC METHOD+ALL/CT  
D QUE L137  
L138 1 SEA ABB=ON L137 AND (L112 OR L113 OR L114 OR L115 OR L116 OR  
L117 OR L109)

FILE 'STNGUIDE' ENTERED AT 12:12:41 ON 05 SEP 2006

D QUE L105  
D QUE L92  
D QUE L79  
D QUE L75  
D QUE L58  
D QUE L59  
D QUE L40  
D QUE L24  
D QUE L27  
D QUE L18

FILE 'CAPLUS' ENTERED AT 12:14:47 ON 05 SEP 2006

D QUE L1  
D QUE L6

L139 9 SEA ABB=ON L1 OR L6

FILE 'WPIX' ENTERED AT 12:14:49 ON 05 SEP 2006

D QUE L31

FILE 'DRUGU, JICST-EPLUS, AGRICOLA, PASCAL, CABA, BIOTECHNO, BIOSIS,  
ESBIOBASE, LIFESCI, CONFSCI, DISSABS, JAPIO, ANABSTR, SCISEARCH' ENTERED  
AT 12:14:50 ON 05 SEP 2006

D QUE L68

FILE 'MEDLINE' ENTERED AT 12:14:52 ON 05 SEP 2006

D QUE L83

FILE 'EMBASE' ENTERED AT 12:14:54 ON 05 SEP 2006

D QUE L110

FILE 'MEDLINE, CAPLUS, WPIX, EMBASE, DRUGU, PASCAL, BIOTECHNO, BIOSIS,  
ESBIOBASE, LIFESCI, CONFSCI, SCISEARCH' ENTERED AT 12:15:12 ON 05 SEP 2006

L140 26 DUP REM L83 L139 L31 L110 L68 (35 DUPLICATES REMOVED)

ANSWERS '1-4' FROM FILE MEDLINE  
ANSWERS '5-10' FROM FILE CAPLUS  
ANSWERS '11-21' FROM FILE BIOSIS  
ANSWER '22' FROM FILE LIFESCI  
ANSWERS '23-24' FROM FILE CONFSCI  
ANSWERS '25-26' FROM FILE SCISEARCH  
D IBIB ED ABS 1-26

FILE 'STNGUIDE' ENTERED AT 12:15:40 ON 05 SEP 2006

D QUE L14  
D QUE L18  
D QUE L30  
D QUE L39  
D QUE L40  
D QUE L71  
D QUE L75

FILE 'CAPLUS' ENTERED AT 12:17:36 ON 05 SEP 2006

D QUE L14

L141 0 SEA ABB=ON L14 NOT L139

FILE 'WPIX' ENTERED AT 12:17:38 ON 05 SEP 2006  
D QUE L30

FILE 'DRUGU, JICST-EPLUS, AGRICOLA, PASCAL, CABA, BIOTECHNO, BIOSIS,  
ESBIOBASE, LIFESCI, CONFSCI, DISSABS, JAPIO, ANABSTR, SCISEARCH' ENTERED  
AT 12:17:40 ON 05 SEP 2006

D QUE L71

L142 0 SEA ABB=ON L71 NOT L68

FILE 'MEDLINE' ENTERED AT 12:17:48 ON 05 SEP 2006  
D QUE L89

FILE 'EMBASE' ENTERED AT 12:17:50 ON 05 SEP 2006  
D QUE L118

FILE 'CAPLUS' ENTERED AT 12:19:00 ON 05 SEP 2006  
D QUE L14

L143 0 SEA ABB=ON L14 NOT L139

FILE 'WPIX' ENTERED AT 12:19:01 ON 05 SEP 2006  
D QUE L30

L144 0 SEA ABB=ON L30 NOT L31

FILE 'DRUGU, JICST-EPLUS, AGRICOLA, PASCAL, CABA, BIOTECHNO, BIOSIS,  
ESBIOBASE, LIFESCI, CONFSCI, DISSABS, JAPIO, ANABSTR, SCISEARCH' ENTERED  
AT 12:19:04 ON 05 SEP 2006

D QUE L71

L145 0 SEA ABB=ON L71 NOT L68

FILE 'MEDLINE' ENTERED AT 12:19:12 ON 05 SEP 2006  
D QUE L89

FILE 'EMBASE' ENTERED AT 12:19:14 ON 05 SEP 2006  
D QUE L118

FILE 'STNGUIDE' ENTERED AT 12:19:27 ON 05 SEP 2006

FILE 'CAPLUS' ENTERED AT 12:20:57 ON 05 SEP 2006  
D QUE L18

L146 3 SEA ABB=ON L18 NOT L139

FILE 'WPIX' ENTERED AT 12:20:58 ON 05 SEP 2006  
D QUE L39

D QUE L40

L147 3 SEA ABB=ON (L39 OR L40) NOT L31

FILE 'DRUGU, JICST-EPLUS, AGRICOLA, PASCAL, CABA, BIOTECHNO, BIOSIS,  
ESBIOBASE, LIFESCI, CONFSCI, DISSABS, JAPIO, ANABSTR, SCISEARCH' ENTERED  
AT 12:21:01 ON 05 SEP 2006

D QUE L75

L148 20 SEA ABB=ON L75 NOT L68

FILE 'MEDLINE' ENTERED AT 12:21:10 ON 05 SEP 2006  
D QUE L92

L149 9 SEA ABB=ON L92 NOT L83

FILE 'EMBASE' ENTERED AT 12:21:12 ON 05 SEP 2006  
D QUE L119

L150 7 SEA ABB=ON L119 NOT L110

FILE 'STNGUIDE' ENTERED AT 12:21:21 ON 05 SEP 2006

FILE 'MEDLINE, CAPLUS, WPIX, EMBASE, BIOTECHNO, BIOSIS, ESBIODBASE, LIFESCI, SCISEARCH' ENTERED AT 12:21:44 ON 05 SEP 2006

L151 28 DUP REM L149 L146 L147 L150 L148 (14 DUPLICATES REMOVED)  
ANSWERS '1-9' FROM FILE MEDLINE  
ANSWERS '10-12' FROM FILE CAPLUS  
ANSWERS '13-15' FROM FILE WPIX  
ANSWERS '16-21' FROM FILE EMBASE  
ANSWERS '22-23' FROM FILE BIOTECHNO  
ANSWERS '24-27' FROM FILE BIOSIS  
ANSWER '28' FROM FILE LIFESCI  
D IALL 1-9  
D IBIB ED ABS HITIND 10-12  
D IALL ABEQ TECH 13-15  
D IALL 16-28

FILE 'STNGUIDE' ENTERED AT 12:22:44 ON 05 SEP 2006

FILE 'CAPLUS' ENTERED AT 12:24:49 ON 05 SEP 2006

D QUE L24  
D QUE L27  
L152 11 SEA ABB=ON (L24 OR L27) NOT (L18 OR L139)

FILE 'WPIX' ENTERED AT 12:24:50 ON 05 SEP 2006

D QUE L58  
D QUE L59  
L153 3 SEA ABB=ON (L58 OR L59) NOT (L39 OR L40 OR L31)

FILE 'DRUGU, JICST-EPLUS, AGRICOLA, PASCAL, CABA, BIOTECHNO, BIOSIS, ESBIODBASE, LIFESCI, CONFSCI, DISSABS, JAPIO, ANABSTR, SCISEARCH' ENTERED AT 12:24:53 ON 05 SEP 2006

D QUE L79  
L154 12 SEA ABB=ON L79 NOT (L75 OR L68)

FILE 'MEDLINE' ENTERED AT 12:25:02 ON 05 SEP 2006

D QUE L105  
L155 10 SEA ABB=ON L105 NOT (L92 OR L83)

FILE 'EMBASE' ENTERED AT 12:25:03 ON 05 SEP 2006

D QUE L138  
L156 1 SEA ABB=ON L138 NOT (L119 OR L110)

FILE 'STNGUIDE' ENTERED AT 12:25:10 ON 05 SEP 2006

FILE 'MEDLINE, CAPLUS, WPIX, EMBASE, DRUGU, PASCAL, BIOTECHNO, ESBIODBASE' ENTERED AT 12:25:33 ON 05 SEP 2006

L157 34 DUP REM L155 L152 L153 L156 L154 (3 DUPLICATES REMOVED)  
ANSWERS '1-10' FROM FILE MEDLINE  
ANSWERS '11-21' FROM FILE CAPLUS  
ANSWERS '22-24' FROM FILE WPIX  
ANSWER '25' FROM FILE EMBASE  
ANSWERS '26-27' FROM FILE DRUGU  
ANSWERS '28-29' FROM FILE BIOTECHNO  
ANSWERS '30-34' FROM FILE ESBIODBASE  
D IALL 1-10  
D IBIB ED ABS HITIND 11-21  
D IALL ABEQ TECH 22-24  
D IALL 25-34



=> fil reg; d ide  
FILE 'REGISTRY' ENTERED AT 09:59:23 ON 05 SEP 2006  
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STRUCTURE FILE UPDATES: 4 SEP 2006 HIGHEST RN 905816-92-4  
DICTIONARY FILE UPDATES: 4 SEP 2006 HIGHEST RN 905816-92-4

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TSCA INFORMATION NOW CURRENT THROUGH June 30, 2006

Please note that search-term pricing does apply when  
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predicted properties as well as tags indicating availability of  
experimental property data in the original document. For information  
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<http://www.cas.org/ONLINE/UG/regprops.html>

L11 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2006 ACS on STN  
RN 372092-80-3 REGISTRY  
ED Entered STN: 28 Nov 2001  
CN Kinase (phosphorylating), protein (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN Neurokinase  
CN Protein kinase  
MF Unspecified  
CI MAN  
SR CA  
LC STN Files: BIOSIS, CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL

\*\*\* STRUCTURE DIAGRAM IS NOT AVAILABLE \*\*\*  
1917 REFERENCES IN FILE CA (1907 TO DATE)  
17 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA  
1930 REFERENCES IN FILE CAPLUS (1907 TO DATE)

=> =>

=>

=> fil capl; d que l1; d que l6

FILE 'CAPLUS' ENTERED AT 12:14:47 ON 05 SEP 2006

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FILE LAST UPDATED: 4 Sep 2006 (20060904/ED)

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'OBI' IS DEFAULT SEARCH FIELD FOR 'CAPLUS' FILE

*Inventor  
search*

L1 1 SEA FILE=CAPLUS ABB=ON US99-235416/PRN

L2 45 SEA FILE=CAPLUS ABB=ON SAKOWICZ R?/AU

L3 1091 SEA FILE=CAPLUS ABB=ON GOLDSTEIN L?/AU

L4 61 SEA FILE=CAPLUS ABB=ON (THERMOMYCES LANUGINOSUS/OBI OR  
TL/OBI) (W) GAMMA/OBI

L6 9 SEA FILE=CAPLUS ABB=ON (L2 AND L3) OR ((L2 OR L3) AND L4)

=> s l1 or l6

L139 9 L1 OR L6

=> fil wpix; d que l31

FILE 'WPIX' ENTERED AT 12:14:49 ON 05 SEP 2006

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FILE LAST UPDATED: 1 SEP 2006 <20060901/UP>

MOST RECENT DERWENT UPDATE: 200656 <200656/DW>

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<http://scientific.thomson.com/media/scpdf/ipcrdwpi.pdf> <<<

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'BI ABEX' IS DEFAULT SEARCH FIELD FOR 'WPIX' FILE

L28 36 SEA FILE=WPIX ABB=ON SAKOWICZ R?/AU  
L29 64 SEA FILE=WPIX ABB=ON GOLDSTEIN L?/AU  
L31 3 SEA FILE=WPIX ABB=ON L28 AND L29

=> fil DRUGU, JICST-EPLUS, AGRICOLA, PASCAL, CABA, BIOTECHNO, BIOSIS,ESBIOBASE,  
LIFESCI, CONFSCI, DISSABS, JAPIO, ANABSTR, SCISEARCH

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FILE 'SCISEARCH' ENTERED AT 12:14:50 ON 05 SEP 2006  
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=> d que 168

L61 138 SEA SAKOWICZ R?/AU  
L62 4782 SEA GOLDSTEIN L?/AU  
L63 147 SEA (THERMOMYCES LANUGINOSUS OR TL) (A) GAMMA  
L68 40 SEA (L61 AND L62) OR ((L61 OR L62) AND L63)

=> fil medl; d que 183

FILE 'MEDLINE' ENTERED AT 12:14:52 ON 05 SEP 2006

FILE LAST UPDATED: 2 Sep 2006 (20060902/UP). FILE COVERS 1950 TO DATE.

On December 11, 2005, the 2006 MeSH terms were loaded.

The MEDLINE reload for 2006 is now (26 Feb.) available. For details  
on the 2006 reload, enter HELP RLOAD at an arrow prompt (=>).  
See also:

<http://www.nlm.nih.gov/mesh/>  
[http://www.nlm.nih.gov/pubs/techbull/nd04/nd04\\_mesh.html](http://www.nlm.nih.gov/pubs/techbull/nd04/nd04_mesh.html)  
[http://www.nlm.nih.gov/pubs/techbull/nd05/nd05\\_med\\_data\\_changes.html](http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_med_data_changes.html)  
[http://www.nlm.nih.gov/pubs/techbull/nd05/nd05\\_2006\\_MeSH.html](http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_2006_MeSH.html)

OLDMEDLINE is covered back to 1950.

MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the  
MeSH 2006 vocabulary.

This file contains CAS Registry Numbers for easy and accurate  
substance identification.

L80 13 SEA FILE=MEDLINE ABB=ON SAKOWICZ R?/AU  
L81 1168 SEA FILE=MEDLINE ABB=ON GOLDSTEIN L?/AU  
L82 11 SEA FILE=MEDLINE ABB=ON (THERMOMYCES LANUGINOSUS OR TL) (A) GAMM  
A  
L83 4 SEA FILE=MEDLINE ABB=ON (L80 AND L81) OR ((L80 OR L81) AND  
L82)

=> fil embase; d que 1110

FILE 'EMBASE' ENTERED AT 12:14:54 ON 05 SEP 2006  
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FILE COVERS 1974 TO 5 Sep 2006 (20060905/ED)

EMBASE has been reloaded. Enter HELP RLOAD for details.

EMBASE is now updated daily. SDI frequency remains weekly (default)  
and biweekly.

This file contains CAS Registry Numbers for easy and accurate  
substance identification.

L107 13 SEA FILE=EMBASE ABB=ON SAKOWICZ R?/AU  
L108 922 SEA FILE=EMBASE ABB=ON GOLDSTEIN L?/AU  
L109 16 SEA FILE=EMBASE ABB=ON (THERMOMYCES LANUGINOSUS OR TL) (A) GAMMA  
  
L110 5 SEA FILE=EMBASE ABB=ON (L107 AND L108) OR ((L107 OR L108) AND  
L109)

=> dup rem l83,l139,l31,l110,l68

FILE 'MEDLINE' ENTERED AT 12:15:12 ON 05 SEP 2006

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PROCESSING COMPLETED FOR L83

PROCESSING COMPLETED FOR L139

PROCESSING COMPLETED FOR L31

PROCESSING COMPLETED FOR L110

PROCESSING COMPLETED FOR L68

L140 26 DUP REM L83 L139 L31 L110 L68 (35 DUPLICATES REMOVED)

ANSWERS '1-4' FROM FILE MEDLINE

ANSWERS '5-10' FROM FILE CAPLUS

ANSWERS '11-21' FROM FILE BIOSIS

ANSWER '22' FROM FILE LIFESCI

ANSWERS '23-24' FROM FILE CONFSCI  
ANSWERS '25-26' FROM FILE SCISEARCH

=> d ibib ed abs 1-26

L140 ANSWER 1 OF 26 MEDLINE on STN DUPLICATE 5  
ACCESSION NUMBER: 2000095847 MEDLINE  
DOCUMENT NUMBER: PubMed ID: 10631986  
TITLE: Cloning and expression of kinesins from the thermophilic fungus *Thermomyces lanuginosus*.  
AUTHOR: Sakowicz R; Farlow S; Goldstein L S  
CORPORATE SOURCE: Howard Hughes Medical Institute, Department of Cellular and Molecular Medicine, School of Medicine, University of California, San Diego, La Jolla 92093-0683, USA.  
CONTRACT NUMBER: GM35252 (NIGMS)  
SOURCE: Protein science : a publication of the Protein Society, (1999 Dec) Vol. 8, No. 12, pp. 2705-10.  
Journal code: 9211750. ISSN: 0961-8368.  
PUB. COUNTRY: United States  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 200002  
ENTRY DATE: Entered STN: 29 Feb 2000  
Last Updated on STN: 29 Feb 2000  
Entered Medline: 14 Feb 2000  
ED Entered STN: 29 Feb 2000  
Last Updated on STN: 29 Feb 2000  
Entered Medline: 14 Feb 2000  
AB The motor domain regions of three novel members of the kinesin superfamily TLKIF1, TLKIFC, and TLBIMC were identified in a thermophilic fungus *Thermomyces lanuginosus*. Based on sequence similarity, they were classified as members of the known kinesin families Unc104/KIF1, KAR3, and BIMC. TLKIF1 was subsequently expressed in *Escherichia coli*. The expression level was high, and the protein was mostly soluble, easy to purify, and enzymatically active. TLKIF1 is a monomeric kinesin motor, which in a gliding motility assay displays a robust plus-directed microtubule movement up to 2 microm/s. The discovery of TLKIF1 also demonstrates that a family of kinesin motors not previously found in fungi may in fact be used in this group of organisms.

L140 ANSWER 2 OF 26 MEDLINE on STN DUPLICATE 7  
ACCESSION NUMBER: 1998202613 MEDLINE  
DOCUMENT NUMBER: PubMed ID: 9535660  
TITLE: A marine natural product inhibitor of kinesin motors.  
AUTHOR: Sakowicz R; Berdelis M S; Ray K; Blackburn C L; Hopmann C; Faulkner D J; Goldstein L S  
CORPORATE SOURCE: Department of Pharmacology, Division of Cellular and Molecular Medicine, Howard Hughes Medical Institute, University of California, San Diego, 9500 Gilman Drive, La Jolla, CA 92093-0683, USA.  
SOURCE: Science, (1998 Apr 10) Vol. 280, No. 5361, pp. 292-5.  
Journal code: 0404511. ISSN: 0036-8075.  
PUB. COUNTRY: United States  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 199804  
ENTRY DATE: Entered STN: 7 May 1998  
Last Updated on STN: 7 May 1998

Entered Medline: 28 Apr 1998

ED Entered STN: 7 May 1998

Last Updated on STN: 7 May 1998

Entered Medline: 28 Apr 1998

AB Members of the kinesin superfamily of motor proteins are essential for mitotic and meiotic spindle organization, chromosome segregation, organelle and vesicle transport, and many other processes that require microtubule-based transport. A compound, adociasulfate-2, was isolated from a marine sponge, Haliclona (also known as Adocia) species, that inhibited kinesin activity by targeting its motor domain and mimicking the activity of the microtubule. Thus, the kinesin-microtubule interaction site could be a useful target for small molecule modulators, and adociasulfate-2 should serve as an archetype for specific inhibitors of kinesin functions.

L140 ANSWER 3 OF 26

MEDLINE on STN

DUPLICATE 9

ACCESSION NUMBER: 1998028574 MEDLINE

DOCUMENT NUMBER: PubMed ID: 9363944

TITLE: CENP-E is a plus end-directed kinetochore motor required for metaphase chromosome alignment.

AUTHOR: Wood K W; Sakowicz R; Goldstein L S; Cleveland D W

CORPORATE SOURCE: Laboratory of Cell Biology, Ludwig Institute for Cancer Research, University of California at San Diego, La Jolla 92093-0660, USA.

SOURCE: Cell, (1997 Oct 31) Vol. 91, No. 3, pp. 357-66.  
Journal code: 0413066. ISSN: 0092-8674.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-AF027728

ENTRY MONTH: 199712

ENTRY DATE: Entered STN: 9 Jan 1998

Last Updated on STN: 9 Jan 1998

Entered Medline: 10 Dec 1997

ED Entered STN: 9 Jan 1998

Last Updated on STN: 9 Jan 1998

Entered Medline: 10 Dec 1997

AB Mitosis requires dynamic attachment of chromosomes to spindle microtubules. This interaction is mediated largely by kinetochores. During prometaphase, forces exerted at kinetochores, in combination with polar ejection forces, drive congression of chromosomes to the metaphase plate. A major question has been whether kinetochore-associated microtubule motors play an important role in congression. Using immunodepletion from and antibody addition to Xenopus egg extracts, we show that the kinetochore-associated kinesin-like motor protein CENP-E is essential for positioning chromosomes at the metaphase plate. We further demonstrate that CENP-E powers movement toward microtubule plus ends in vitro. These findings support a model in which CENP-E functions in congression to tether kinetochores to dynamic microtubule plus ends.

L140 ANSWER 4 OF 26

MEDLINE on STN

ACCESSION NUMBER: 96196874 MEDLINE

DOCUMENT NUMBER: PubMed ID: 8612068

TITLE: The muscle in kinesin.

AUTHOR: Sakowicz R; Goldstein L S

SOURCE: Nature structural biology, (1996 May) Vol. 3, No. 5, pp. 404-7.

Journal code: 9421566. ISSN: 1072-8368.

PUB. COUNTRY: United States  
 DOCUMENT TYPE: News Announcement  
 LANGUAGE: English  
 FILE SEGMENT: Priority Journals  
 ENTRY MONTH: 199606  
 ENTRY DATE: Entered STN: 13 Jun 1996  
 Last Updated on STN: 13 Jun 1996  
 Entered Medline: 3 Jun 1996

ED Entered STN: 13 Jun 1996  
 Last Updated on STN: 13 Jun 1996  
 Entered Medline: 3 Jun 1996

L140 ANSWER 5 OF 26 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 1

ACCESSION NUMBER: 1999:487304 CAPLUS  
 DOCUMENT NUMBER: 131:112405  
 TITLE: Identification and expression of the microtubule motor protein kinesin TL- $\gamma$   
 INVENTOR(S): Sakowicz, Roman; Goldstein, Lawrence S. B.  
 PATENT ASSIGNEE(S): The Regents of the University of California, USA  
 SOURCE: PCT Int. Appl., 75 pp.  
 CODEN: PIXXD2  
 DOCUMENT TYPE: Patent  
 LANGUAGE: English  
 FAMILY ACC. NUM. COUNT: 1  
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9937659	A1	19990729	WO 1999-US1355	19990122
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 9924648	A1	19990809	AU 1999-24648	19990122
US 6723840	B1	20040420	US 2000-724586	20001128 <--
US 6815169	B1	20041109	US 2000-724666	20001128 <--
US 6764830	B1	20040720	US 2000-600823	20001221 <--
PRIORITY APPLN. INFO.:			US 1998-72361P	A2 19980123
			US 1999-235416	A3 19990122 <--
			WO 1999-US1355	W 19990122

ED Entered STN: 06 Aug 1999

AB The invention concerns the isolation of a nucleic acid sequence from *Thermomyces lanuginosus* that encodes the microtubule motor protein kinesin TL- $\gamma$  with the following properties: the protein's activity includes plus end-directed microtubule motor activity; the protein has a tail domain that has greater than 60% amino acid sequence identity to a TL- $\gamma$  tail domain as measured using a sequence comparison algorithm; the protein specifically binds to polyclonal antibodies to TL- $\gamma$ . The invention also concerns antibodies to TL- $\gamma$ , methods for screening biol. active TL- $\gamma$ , and kits for screening. Using PCR and degenerate primers, TL- $\gamma$  was amplified from *Thermomyces lanuginosus* genomic DNA. The nucleic acid sequence was then used as a probe to isolate a longer TL- $\gamma$  sequence. Recombinant TL- $\gamma$  was prepared in order to test its activity in a microtubule gliding assay. The



pET23-TL- $\gamma$  expression vector was constructed and expressed in *E. coli*. The kinesin TL- $\gamma$  protein was isolated, it was very stable retaining 100% activity up to 40° after incubation for 15 min as measured using a microtubule dependent ATPase assay. Freshly prepared protein was used to assay microtubule gliding activity. Taxol stabilized microtubule seeds brightly labeled with rhodamine were prepared by incubating a 1:1 ratio of rhodamine labeled bovine brain tubulin; also unlabeled bovine brain tubulin was incorporated into the assay. Flow chambers prepared were preadsorbed with TL- $\gamma$  motor protein. A microtubule/ATP mix containing polarity marked microtubules, taxol, MgATP and an oxygen scavenging system was then flowed into the chamber. Movement of microtubules was monitored at room temperature on a fluorescence microscope fitted with oil immersion objective and a CCD. For TL- $\gamma$  activity measurement, recombinant TL- $\gamma$  protein was attached to a glass coverslip using non-specific adhesion, and gliding of polarity marked microtubules containing brightly fluorescent rhodamine labeled seeds near their minus ends was recorded by time-lapse digital fluorescence microscopy. Microtubules moved with brightly fluorescent seeds leading, indicating that the immobilized TL- $\gamma$  protein was moving toward microtubule plus ends. No movement was observed in the absence of TL- $\gamma$ . This experiment demonstrates that TL- $\gamma$  has plus-ended microtubule motor activity.

REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L140 ANSWER 6 OF 26 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 2

ACCESSION NUMBER: 1999:451195 CAPLUS

DOCUMENT NUMBER: 131:97592

TITLE: Kinesin motor modulators derived from the marine sponge adocia

INVENTOR(S): Goldstein, Lawrence S. B.; Faulkner, David John; Sakowicz, Roman; Berdelis, Michael S.; Blackburn, Christine L.; Hopmann, Cordula

PATENT ASSIGNEE(S): The Regents of the University of California, USA

SOURCE: PCT Int. Appl., 73 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9934806	A1	19990715	WO 1999-US321	19990106
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 9921071	A1	19990726	AU 1999-21071	19990106
EP 1049475	A1	20001108	EP 1999-901353	19990106
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
US 6207403	B1	20010327	US 1999-226772	19990106
JP 2002500190	T2	20020108	JP 2000-527255	19990106
US 6489134	B1	20021203	US 2000-724609	20001128

US 2003127621	A1	20030710	US 2002-305857	20021127
US 6777200	B2	20040817		
US 2004176625	A1	20040909	US 2004-794757	20040303
PRIORITY APPLN. INFO.:			US 1998-70772P	P 19980108
			US 1999-226772	A3 19990106
			WO 1999-US321	W 19990106
			US 2000-724609	A1 20001128
			US 2002-305857	A1 20021127

OTHER SOURCE(S): MARPAT 131:97592

ED Entered STN: 23 Jul 1999

AB This invention provides novel compds. derived from a marine sponge, Adocia sp., that specifically modulate kinesin activity by targeting the kinesin motor domain and mimicking the activity of a microtubule. The compds. act as potent anti-mitogens and are useful in a wide variety of in vitro and in vivo applications [e.g. in mitigating a variety of pathol. conditions characterized by abnormal cell mitosis].

REFERENCE COUNT: 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L140 ANSWER 7 OF 26 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 3

ACCESSION NUMBER: 1999:194248 CAPLUS

DOCUMENT NUMBER: 130:233824

TITLE: Plus end-directed microtubule motor protein CENP-E required for Xenopus chromosome congression

INVENTOR(S): Wood, Kenneth W.; Sakowicz, Roman; Goldstein, Lawrence S. B.; Cleveland, Don W.

PATENT ASSIGNEE(S): The Regents of the University of California, USA

SOURCE: PCT Int. Appl., 78 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9913061	A1	19990318	WO 1998-US19231	19980910
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
CA 2303484	AA	19990318	CA 1998-2303484	19980910
AU 9893918	A1	19990329	AU 1998-93918	19980910
AU 745385	B2	20020321		
EP 1012249	A1	20000628	EP 1998-947039	19980910
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2001526881	T2	20011225	JP 2000-510850	19980910
US 6645748	B1	20031111	US 1998-150867	19980910
US 7009043	B1	20060307	US 2000-724584	20001128
US 2005191631	A1	20050901	US 2003-650280	20030827
PRIORITY APPLN. INFO.:			US 1997-58645P	P 19970911
			US 1998-150867	A1 19980910
			WO 1998-US19231	W 19980910

ED Entered STN: 25 Mar 1999

AB The invention provides isolated nucleic acid and amino acid sequences of

Xenopus centromere-associated protein-E (XCENP-E), antibodies to XCENP-E, methods of screening for CENP-E modulators using biol. active CENP-E, and kits for screening for CENP-E modulators. The full-length cDNA sequences of XCENP-E encodes a protein of 2954 amino acids with a predicted mol. mass of 340 kDa. XCENP-E is a member of the kinesin superfamily of motor proteins, and consists of a 500-amino acid globular N-terminal domain containing a kinesin-like microtubule motor domain linked to a globular tail domain by a region predicted to form a long, discontinuous  $\alpha$ -helical coiled coil. This is the first biol. active CENP-E isolated and, surprisingly and contrary to previous reports, it demonstrates a motor that powers chromosome movement toward microtubule plus ends. Using immunodepletion and antibody addition to Xenopus egg exts., the present invention further demonstrates that CENP-E plays an essential role in congression.

REFERENCE COUNT: 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L140 ANSWER 8 OF 26 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 4

ACCESSION NUMBER: 1999:420033 CAPLUS

DOCUMENT NUMBER: 131:211782

TITLE: Adociasulfates 1-6, inhibitors of kinesin motor proteins from the sponge Haliclona (aka Adocia) sp.

AUTHOR(S): Blackburn, Christine L.; Hopmann, Cordula;

Sakowicz, Roman; Berdelis, Michael S.;

Goldstein, Lawrence S. B.; Faulkner, D. John

CORPORATE SOURCE: Scripps Institution of Oceanography, University of California at San Diego, La Jolla, CA, 92093-0212, USA

SOURCE: Journal of Organic Chemistry (1999), 64(15), 5565-5570

CODEN: JOCEAH; ISSN: 0022-3263

PUBLISHER: American Chemical Society

DOCUMENT TYPE: Journal

LANGUAGE: English

ED Entered STN: 08 Jul 1999

GI

\* STRUCTURE DIAGRAM TOO LARGE FOR DISPLAY - AVAILABLE VIA OFFLINE PRINT \*

AB Adociasulfates 1-6 were isolated from an extract of the Palauan sponge Haliclona (aka Adocia) sp. that inhibited the transport of stabilized microtubules by the motor protein kinesin, which was immobilized on a microscope slide. The structures of adociasulfates 1-6, the relative stereochem. of adociasulfates 1 (I), 2, 5, and 6, and the relative stereochem. of subunits of adociasulfates 3 (II) and 4 were determined by interpretation of spectroscopic data. In a quant. assay that measures ATP hydrolysis by kinesin, adociasulfates 2 and 6 were the most active.

REFERENCE COUNT: 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L140 ANSWER 9 OF 26 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 10

ACCESSION NUMBER: 1996:282241 CAPLUS

DOCUMENT NUMBER: 124:310323

TITLE: The muscle in kinesin

AUTHOR(S): Sakowicz, Roman; Goldstein, Lawrence S.

B.

CORPORATE SOURCE: Howard Hughes Medical Inst., Univ. California, La Jolla, CA, 92093-0683, USA

SOURCE: Nature Structural Biology (1996), 3(5), 404-407

CODEN: NSBIEW; ISSN: 1072-8368  
PUBLISHER: Nature Publishing Co.  
DOCUMENT TYPE: Journal; General Review  
LANGUAGE: English  
ED Entered STN: 14 May 1996  
AB A review, with 41 refs. The first high resolution structures of the kinesin and NCD motor proteins reveal their surprising similarity to myosin but leave open the tantalizing question of what properties eet. the directionality of movement along microtubules.

L140 ANSWER 10 OF 26 CAPLUS COPYRIGHT 2006 ACS on STN DUPLICATE 11  
ACCESSION NUMBER: 1997:151799 CAPLUS  
DOCUMENT NUMBER: 126:234999  
TITLE: Single molecules solvated in pores of polyacrylamide gels  
AUTHOR(S): Dickson, Robert M.; Norris, D. J.; Tzeng, Yih-Ling; Sakowicz, R.; Goldstein, L. S. B.; Moerner, W. E.  
CORPORATE SOURCE: Department Chemistry Biochemistry, University California San Diego, La Jolla, CA, 92093-0340, USA  
SOURCE: Molecular Crystals and Liquid Crystals Science and Technology, Section A: Molecular Crystals and Liquid Crystals (1996), 291, 31-39  
CODEN: MCLCE9; ISSN: 1058-725X  
PUBLISHER: Gordon & Breach  
DOCUMENT TYPE: Journal  
LANGUAGE: English

ED Entered STN: 08 Mar 1997  
AB Individual fluorescent mols. and individual singly-labeled proteins have been observed in the water-filled pores of poly(acrylamide) gels with far-field microscopy. The mol. range of motion is dramatically reduced by the gel framework, thus allowing single mols. to be studied in an aqueous environment for long periods of time. For the small fluorophores, the gel restricts Brownian motion by approx. two orders of magnitude in each direction, thus greatly enhancing the mol.'s detectability. In contrast to dry polymeric hosts, the gel is composed primarily of water and the majority of mols. remain in solution, thus making these gels an ideal medium in which to utilize single mol. detection methods for the study of biol. systems in vitro.

L140 ANSWER 11 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN DUPLICATE 6  
ACCESSION NUMBER: 1999:185585 BIOSIS  
DOCUMENT NUMBER: PREV199900185585  
TITLE: Single-molecule studies of fluorescent proteins and enzymes.  
AUTHOR(S): Moerner, W. E. [Reprint author]; Peterman, E. J.; Sosa, H.; Brasselet, S.; Dickson, R. M.; Kummer, S.; Sakowicz, R.; Goldstein, L. S. B.  
CORPORATE SOURCE: Department of Chemistry, Stanford University, Stanford, CA, USA  
SOURCE: Biophysical Journal, (Jan., 1999) Vol. 76, No. 1 PART 2, pp. A20. print.  
Meeting Info.: Forty-third Annual Meeting of the Biophysical Society. Baltimore, Maryland, USA. February 13-17, 1999.  
CODEN: BIOJAU. ISSN: 0006-3495.  
DOCUMENT TYPE: Conference; (Meeting)  
Conference; Abstract; (Meeting Abstract)  
LANGUAGE: English

ENTRY DATE: Entered STN: 5 May 1999  
Last Updated on STN: 5 May 1999  
ED Entered STN: 5 May 1999  
Last Updated on STN: 5 May 1999

L140 ANSWER 12 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on  
STN DUPLICATE 8

ACCESSION NUMBER: 1999:15470 BIOSIS  
DOCUMENT NUMBER: PREV199900015470  
TITLE: Study of the orientation of kinesin motors bound to  
microtubules using single molecule fluorescence  
polarization spectroscopy.  
AUTHOR(S): Sosa, H. [Reprint author]; Peterman, E. J. G.; Dickson, R.  
M.; Sakowicz, R.; Moerner, W. E.; Goldstein,  
L. G.  
CORPORATE SOURCE: Dep. Pharmacology, Univ. Calif., San Diego, CA 92093, USA  
SOURCE: Molecular Biology of the Cell, (Nov., 1998) Vol. 9, No.  
SUPPL., pp. 28A. print.  
Meeting Info.: 38th Annual Meeting of the American Society  
for Cell Biology. San Francisco, California, USA. December  
12-16, 1998. American Society for Cell Biology.  
CODEN: MBCEEV. ISSN: 1059-1524.  
DOCUMENT TYPE: Conference; (Meeting)  
Conference; Abstract; (Meeting Abstract)  
LANGUAGE: English  
ENTRY DATE: Entered STN: 20 Jan 1999  
Last Updated on STN: 20 Jan 1999  
ED Entered STN: 20 Jan 1999  
Last Updated on STN: 20 Jan 1999

L140 ANSWER 13 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on  
STN

ACCESSION NUMBER: 2006:342933 BIOSIS  
DOCUMENT NUMBER: PREV200600349154  
TITLE: Plus end-directed microtubule motor required for chromosome  
congression.  
AUTHOR(S): Wood, Kenneth W. [Inventor]; Sakowicz, Roman  
[Inventor]; Goldstein, Lawrence S. B. [Inventor];  
Cleveland, Don W. [Inventor]  
CORPORATE SOURCE: Foster City, CA USA  
ASSIGNEE: The Regents of the University of California  
PATENT INFORMATION: US 07009043 20060307  
SOURCE: Official Gazette of the United States Patent and Trademark  
Office Patents, (MAR 7 2006)  
CODEN: OGUPE7. ISSN: 0098-1133.  
DOCUMENT TYPE: Patent  
LANGUAGE: English  
ENTRY DATE: Entered STN: 12 Jul 2006  
Last Updated on STN: 12 Jul 2006

ED Entered STN: 12 Jul 2006  
Last Updated on STN: 12 Jul 2006  
AB The invention provides isolated nucleic acid and amino acid sequences of  
Xenopus CENP-E (XCENP-E), antibodies to XCENP-E, methods of screening for  
CENP-E modulators using biologically active CENP-E, and kits for screening  
for CENP-E modulators.

L140 ANSWER 14 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on  
STN

ACCESSION NUMBER: 2004:468880 BIOSIS  
DOCUMENT NUMBER: PREV200400473914

TITLE: Identification and expression of a novel kinesin motor protein.  
AUTHOR(S): Sakowicz, Roman [Inventor, Reprint Author]; Goldstein, Lawrence S. B. [Inventor]  
CORPORATE SOURCE: ASSIGNEE: The Regents of the University of California  
PATENT INFORMATION: US 6815169 20041109  
SOURCE: Official Gazette of the United States Patent and Trademark Office Patents, (Nov 9 2004) Vol. 1288, No. 2.  
<http://www.uspto.gov/web/menu/patdata.html>. e-file.  
ISSN: 0098-1133 (ISSN print).  
DOCUMENT TYPE: Patent  
LANGUAGE: English  
ENTRY DATE: Entered STN: 9 Dec 2004  
Last Updated on STN: 9 Dec 2004  
ED Entered STN: 9 Dec 2004  
Last Updated on STN: 9 Dec 2004  
AB The invention provides isolated nucleic acid and amino acid sequences of **TL-gamma**, antibodies to **TL-gamma**, methods of screening for **TL-gamma** modulators using biologically active **TL-gamma**, and kits for screening for **TL-gamma** modulators.

L140 ANSWER 15 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN  
ACCESSION NUMBER: 2004:376082 BIOSIS  
DOCUMENT NUMBER: PREV200400381987  
TITLE: Kinesin motor modulators derived from the marine sponge Adocia.  
AUTHOR(S): Goldstein, Lawrence S. B. [Inventor, Reprint Author]; Faulkner, David John [Inventor]; Sakowicz, Roman [Inventor]; Berdelis, Michael S. [Inventor]; Blackburn, Christine L. [Inventor]; Hopmann, Cordula [Inventor]  
CORPORATE SOURCE: Frankfurt am Main, Germany  
ASSIGNEE: The Regents of the University of California  
PATENT INFORMATION: US 6777200 20040817  
SOURCE: Official Gazette of the United States Patent and Trademark Office Patents, (Aug 17 2004) Vol. 1285, No. 3.  
<http://www.uspto.gov/web/menu/patdata.html>. e-file.  
ISSN: 0098-1133 (ISSN print).  
DOCUMENT TYPE: Patent  
LANGUAGE: English  
ENTRY DATE: Entered STN: 22 Sep 2004  
Last Updated on STN: 22 Sep 2004  
ED Entered STN: 22 Sep 2004  
Last Updated on STN: 22 Sep 2004  
AB This invention provides novel compounds derived from a marine sponge, Adocia sp., that specifically modulate kinesin activity by targeting the kinesin motor domain and mimicking the activity of a microtubule. The compounds act as potent anti-mitogens and are useful in a wide variety of in vitro and in vivo applications.

L140 ANSWER 16 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN  
ACCESSION NUMBER: 2004:332625 BIOSIS  
DOCUMENT NUMBER: PREV200400337426  
TITLE: Thermomyces lanuginosus kinesin motor protein and methods of screening for modulators of kinesin proteins.  
AUTHOR(S): Sakowicz, Roman [Inventor, Reprint Author]; Goldstein, Lawrence S. B. [Inventor]

CORPORATE SOURCE: ASSIGNEE: The Regents of the University of California  
PATENT INFORMATION: US 6764830 20040720  
SOURCE: Official Gazette of the United States Patent and Trademark  
Office Patents, (July 20 2004) Vol. 1284, No. 3.  
<http://www.uspto.gov/web/menu/patdata.html>. e-file.  
ISSN: 0098-1133 (ISSN print).

DOCUMENT TYPE: Patent  
LANGUAGE: English  
ENTRY DATE: Entered STN: 4 Aug 2004  
Last Updated on STN: 4 Aug 2004

ED Entered STN: 4 Aug 2004

Last Updated on STN: 4 Aug 2004

AB The invention provides isolated nucleic acid and amino acid sequences of  
**TL-gamma**, antibodies to **TL-gamma**,  
methods of screening for **TL-gamma** modulating using  
biologically active **TL-gamma**, and kits for screening  
for **TL-gamma** modulators.

L140 ANSWER 17 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on  
STN

ACCESSION NUMBER: 2004:7637 BIOSIS

DOCUMENT NUMBER: PREV200400008401

TITLE: Plus end-directed microtubule motor required for chromosome  
congression.

AUTHOR(S): Wood, Kenneth W. [Inventor, Reprint Author]; **Sakowicz,**  
**Roman** [Inventor]; **Goldstein, Lawrence S. B.**  
[Inventor]; Cleveland, Don W. [Inventor]

CORPORATE SOURCE: Delmar, CA, USA

ASSIGNEE: The Regents of the University of California

PATENT INFORMATION: US 6645748 20031111

SOURCE: Official Gazette of the United States Patent and Trademark  
Office Patents, (Nov 11 2003) Vol. 1276, No. 2.  
<http://www.uspto.gov/web/menu/patdata.html>. e-file.  
ISSN: 0098-1133 (ISSN print).

DOCUMENT TYPE: Patent

LANGUAGE: English

ENTRY DATE: Entered STN: 17 Dec 2003

Last Updated on STN: 17 Dec 2003

ED Entered STN: 17 Dec 2003

Last Updated on STN: 17 Dec 2003

AB The invention provides isolated nucleic acid and amino acid sequences of  
Xenopus CENP-E (XCENP-E), antibodies to XCENP-E, methods of screening for  
CENP-E modulators using biologically active CENP-E, and kits for screening  
for CENP-E modulators.

L140 ANSWER 18 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on  
STN

ACCESSION NUMBER: 2003:56963 BIOSIS

DOCUMENT NUMBER: PREV200300056963

TITLE: Kinesin motor modulators derived from the marine sponge  
Adocia.

AUTHOR(S): **Goldstein, Lawrence S.B.** [Inventor, Reprint  
Author]; Faulkner, David John [Inventor]; **Sakowicz,**  
**Roman** [Inventor]; Berdelis, Michael S. [Inventor];  
Blackburn, Christine L. [Inventor]; Hopmann, Cordula  
[Inventor]

CORPORATE SOURCE: San Diego, CA, USA

ASSIGNEE: The Regents of the University of California

PATENT INFORMATION: US 6489134 20021203

SOURCE: Official Gazette of the United States Patent and Trademark

Office Patents, (Dec 3 2002) Vol. 1265, No. 1.  
<http://www.uspto.gov/web/menu/patdata.html>. e-file.  
ISSN: 0098-1133 (ISSN print).

DOCUMENT TYPE: Patent  
LANGUAGE: English  
ENTRY DATE: Entered STN: 22 Jan 2003  
Last Updated on STN: 22 Jan 2003

ED Entered STN: 22 Jan 2003

Last Updated on STN: 22 Jan 2003

AB This invention provides novel compounds derived from a marine sponge, Adocia sp., that specifically modulate kinesin activity by targeting the kinesin motor domain and mimicking the activity of a microtubule. The compounds act as potent anti-mitogens and are useful in a wide variety of in vitro and in vivo applications.

L140 ANSWER 19 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN

ACCESSION NUMBER: 2001:461909 BIOSIS

DOCUMENT NUMBER: PREV200100461909

TITLE: Kinesin motor modulators derived from the marine sponge Adocia.

AUTHOR(S): Goldstein, Lawrence S. B. [Inventor, Reprint author]; Faulkner, David John [Inventor]; Sakowicz, Roman [Inventor]; Berdelis, Michael S. [Inventor]; Blackburn, Christine L. [Inventor]; Hopmann, Cordula [Inventor]

CORPORATE SOURCE: San Diego, CA, USA

ASSIGNEE: The Regents of the University of California

PATENT INFORMATION: US 6207403 20010327

SOURCE: Official Gazette of the United States Patent and Trademark Office Patents, (Mar. 27, 2001) Vol. 1244, No. 4. e-file.  
CODEN: OGUPE7. ISSN: 0098-1133.

DOCUMENT TYPE: Patent  
LANGUAGE: English  
ENTRY DATE: Entered STN: 3 Oct 2001  
Last Updated on STN: 22 Feb 2002

ED Entered STN: 3 Oct 2001

Last Updated on STN: 22 Feb 2002

AB This invention provides novel compounds derived from a marine sponge, Adocia sp., that specifically modulate kinesin activity by targeting the kinesin motor domain and mimicking the activity of a microtubule. The compounds act as potent anti-mitogens and are useful in a wide variety of in vitro and in vivo applications.

L140 ANSWER 20 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN

ACCESSION NUMBER: 1998:20152 BIOSIS

DOCUMENT NUMBER: PREV199800020152

TITLE: CENP-E is a plus end-directed kinetochore motor required for chromosome congression.

AUTHOR(S): Wood, K. W. [Reprint author]; Sakowicz, R.; Goldstein, L. S. B.; Cleveland, D. W. [Reprint author]

CORPORATE SOURCE: Lab. Cell Biol., Ludwig Inst. Cancer Research, La Jolla, CA 92093-0660, USA

SOURCE: Molecular Biology of the Cell, (Nov., 1997) Vol. 8, No. SUPPL., pp. 125A. print.  
Meeting Info.: 37th Annual Meeting of the American Society for Cell Biology. Washington, D.C., USA. December 13-17, 1997. American Society for Cell Biology.



CODEN: MBCEEV. ISSN: 1059-1524.  
DOCUMENT TYPE: Conference; (Meeting)  
Conference; Abstract; (Meeting Abstract)  
LANGUAGE: English  
ENTRY DATE: Entered STN: 5 Jan 1998  
Last Updated on STN: 5 Jan 1998  
ED Entered STN: 5 Jan 1998  
Last Updated on STN: 5 Jan 1998

L140 ANSWER 21 OF 26 BIOSIS COPYRIGHT (c) 2006 The Thomson Corporation on STN

ACCESSION NUMBER: 1997:95559 BIOSIS  
DOCUMENT NUMBER: PREV199799394762  
TITLE: Cloning, expression, and purification of kinesin superfamily members from the thermophilic fungus.  
AUTHOR(S): Sakowicz, R.; Farlow, S.; Goldstein, L. S. B.  
CORPORATE SOURCE: Howard Hughes Med. Inst., Div. Cell. Mol. Med., Dep. Pharmacol., Univ. Calif. San Diego, 9500 Gilman Dr., La Jolla, CA 92093-0683, USA  
SOURCE: Molecular Biology of the Cell, (1996) Vol. 7, No. SUPPL., pp. 215A.  
Meeting Info.: Annual Meeting of the 6th International Congress on Cell Biology and the 36th American Society for Cell Biology. San Francisco, California, USA. December 7-11, 1996.  
CODEN: MBCEEV. ISSN: 1059-1524.  
DOCUMENT TYPE: Conference; (Meeting)  
Conference; Abstract; (Meeting Abstract)  
Conference; (Meeting Poster)  
LANGUAGE: English  
ENTRY DATE: Entered STN: 3 Mar 1997  
Last Updated on STN: 3 Mar 1997  
ED Entered STN: 3 Mar 1997  
Last Updated on STN: 3 Mar 1997

L140 ANSWER 22 OF 26 LIFESCI COPYRIGHT 2006 CSA on STN

ACCESSION NUMBER: 2003:77194 LIFESCI  
TITLE: Kinesin motor modulators derived from the marine sponge Adocia  
AUTHOR: Goldstein, L.S.B.; Faulkner, D.J.; Sakowicz, R.; Berdelis, M.S.; Blackburn, C.L.; Hopmann, C.  
CORPORATE SOURCE: The Regents of the University of California, Oakland, California  
SOURCE: (20021203) . US Patent: 6489134; US CLASS: 435/21; 435/6; 514/172; 514/182; 514/518; 585/350.  
DOCUMENT TYPE: Patent  
FILE SEGMENT: Q4  
LANGUAGE: English  
SUMMARY LANGUAGE: English

AB This invention provides novel compounds derived from a marine sponge, Adocia sp., that specifically modulate kinesin activity by targeting the kinesin motor domain and mimicking the activity a microtubule. The compounds act as potent anti-mitogens are useful in a wide variety of in vitro and in vivo applications.

L140 ANSWER 23 OF 26 CONFSCI COPYRIGHT 2006 CSA on STN

ACCESSION NUMBER: 1999:35078 CONFSCI  
DOCUMENT NUMBER: 99-047572  
TITLE: Single-molecule studies of fluorescent proteins and

enzymes. Topic(s): 09A 01D  
AUTHOR: Moerner, W.E.; Peterman, E.J.; Sosa, H.; Brasselet, S.;  
Dickson, R.M.; Kummer, S.; Sakowicz, R.;  
Goldstein, L.S.B.  
CORPORATE SOURCE: Stanford Univ., USA  
SOURCE: Biophysical Society, 9650 Rockville Pike, Bethesda, MD  
20814, USA; phone: (301) 530-7114; fax: (301) 530-7133;  
email: society@biophysics.faseb.org; URL:  
www.biophysics.faseb.org, Abstracts available. Price \$25..  
Meeting Info.: 991 0048: 43rd Annual Meeting of the  
Biophysical Society (9910048). Baltimore, MD (USA). 13-17  
Feb 1999. Biophysical Society.  
DOCUMENT TYPE: Conference  
FILE SEGMENT: DCCP  
LANGUAGE: English

L140 ANSWER 24 OF 26 CONFSCI COPYRIGHT 2006 CSA on STN  
ACCESSION NUMBER: 1999:26143 CONFSCI  
DOCUMENT NUMBER: 99-038637  
TITLE: Study of the orientation of kinesin motors bound to  
microtubules using single molecule fluorescence  
polarization spectroscopy  
AUTHOR: Sosa, H.; Peterman, E.J.G.; Dickson, R.M.; Sakowicz,  
R.; Moerner, W.E.; Goldstein, L.G.  
CORPORATE SOURCE: Dep. Pharmacol., Univ. California at San Diego, CA 92093,  
USA  
SOURCE: American Society for Cell Biology, 9650 Rockville Pike,  
Bethesda, MD 20814, USA; phone: (301) 530-7153; fax: (301)  
530-7139; email: ascbinfo@ascb.org; URL:  
www.ascb.org/ascb/, Abstracts available. Price \$45. Paper  
No. 159.  
Meeting Info.: 984 0478: 38th American Society for Cell  
Biology Annual Meeting (9840478). San Francisco, CA (USA).  
12-16 Dec 1998. ASCB, Bio-Rad, Genentech, Jeol USA, Johnson  
& Johnson, Leica, Leadership Alliance, Mark-Rambar Family  
Foundation.  
DOCUMENT TYPE: Conference  
FILE SEGMENT: DCCP  
LANGUAGE: English

L140 ANSWER 25 OF 26 SCISEARCH COPYRIGHT (c) 2006 The Thomson Corporation on  
STN  
ACCESSION NUMBER: 1997:848661 SCISEARCH  
THE GENUINE ARTICLE: YF096  
TITLE: CENP-E is a plus end-directed kinetochore motor required  
for chromosome congression  
AUTHOR: Wood K W (Reprint); Sakowicz R; Goldstein L  
S B; Cleveland D W  
CORPORATE SOURCE: UNIV CALIF SAN DIEGO, CELL BIOL LAB, LUDWIG INST CANC RES,  
LA JOLLA, CA 92093; UNIV CALIF SAN DIEGO, HOWARD HUGHES  
MED INST, DIV CELLULAR & MOL MED, LA JOLLA, CA 92093  
COUNTRY OF AUTHOR: USA  
SOURCE: MOLECULAR BIOLOGY OF THE CELL, (NOV 1997) Vol. 8, Supp.  
[S], pp. 723-723.  
ISSN: 1059-1524.  
PUBLISHER: AMER SOC CELL BIOLOGY, 8120 WOODMONT AVE, STE 750,  
BETHESDA, MD 20814-2755 USA.  
DOCUMENT TYPE: Conference; Journal  
LANGUAGE: English  
REFERENCE COUNT: 0

ENTRY DATE: Entered STN: 1997  
Last Updated on STN: 1997

ED Entered STN: 1997  
Last Updated on STN: 1997

L140 ANSWER 26 OF 26 SCISEARCH COPYRIGHT (c) 2006 The Thomson Corporation on  
STN

ACCESSION NUMBER: 1997:46229 SCISEARCH

THE GENUINE ARTICLE: WB018

TITLE: Cloning, expression, and purification of kinesin  
superfamily members from the thermophilic fungus.

AUTHOR: Sakowicz R (Reprint); Farlow S; Goldstein L  
S B

CORPORATE SOURCE: UNIV CALIF SAN DIEGO, DEPT PHARMACOL, DIV CELLULAR & MOL  
MED, HOWARD HUGHES MED INST, LA JOLLA, CA 92093

COUNTRY OF AUTHOR: USA

SOURCE: MOLECULAR BIOLOGY OF THE CELL, (DEC 1996) Vol. 7, Supp.  
[S], pp. 1250-1250.  
ISSN: 1059-1524.

PUBLISHER: AMER SOC CELL BIOLOGY, 8120 WOODMONT AVE, STE 750,  
BETHESDA, MD 20814-2755 USA.

DOCUMENT TYPE: Conference; Journal

LANGUAGE: English

REFERENCE COUNT: 0

ENTRY DATE: Entered STN: 1997  
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Last Updated on STN: 1997

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L5 17063 SEA FILE=CAPLUS ABB=ON TEST KITS/CT  
L7 1841 SEA FILE=CAPLUS ABB=ON KINESINS/CT  
L9 20619 SEA FILE=CAPLUS ABB=ON MICROTUBULE#/OBI  
L10 3352 SEA FILE=CAPLUS ABB=ON MOTOR/OBI (L) PROTEIN#/OBI  
L11 1 SEA FILE=REGISTRY ABB=ON "PROTEIN KINASE"/CN  
L12 97768 SEA FILE=CAPLUS ABB=ON L11 OR PROTEIN KINASE#/OBI  
L14 1 SEA FILE=CAPLUS ABB=ON L4 AND (L5 OR L7 OR L9 OR L10 OR L12)

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L143

0 L14 NOT

L139

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[http://www.stn-international.de/stndatabases/details/dwpi\\_r.html](http://www.stn-international.de/stndatabases/details/dwpi_r.html) <<<  
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                         TL/BI,ABEX) (A) GAMMA/BI,ABEX

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L144

0 L30 NOT L31

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=> d que 171

L63 147 SEA (THERMOMYCES LANUGINOSUS OR TL) (A) GAMMA  
L64 13861 SEA KINESIN#  
L65 132140 SEA MICROTUBULE# OR MICRO TUBULE#  
L66 7756 SEA MOTOR PROTEIN#  
L67 2654 SEA END DIRECT?  
L70 567385 SEA PROTEIN KINASE#  
L71 3 SEA L63 AND (L64 OR L65 OR L66 OR L67 OR L70)

=> s 171 not 168

L145

0 L71 NOT L68

*previously printed*

=> fil medl; d que 189

FILE 'MEDLINE' ENTERED AT 12:19:12 ON 05 SEP 2006

FILE LAST UPDATED: 2 Sep 2006 (20060902/UP). FILE COVERS 1950 TO DATE.

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<http://www.nlm.nih.gov/mesh/>  
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[http://www.nlm.nih.gov/pubs/techbull/nd05/nd05\\_med\\_data\\_changes.html](http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_med_data_changes.html)  
[http://www.nlm.nih.gov/pubs/techbull/nd05/nd05\\_2006\\_MeSH.html](http://www.nlm.nih.gov/pubs/techbull/nd05/nd05_2006_MeSH.html)

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MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the MeSH 2006 vocabulary.

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L82 11 SEA FILE=MEDLINE ABB=ON (THERMOMYCES LANUGINOSUS OR TL) (A) GAMMA  
A  
L84 2094 SEA FILE=MEDLINE ABB=ON KINESIN/CT  
L85 17967 SEA FILE=MEDLINE ABB=ON MICROTUBULES/CT  
L86 76212 SEA FILE=MEDLINE ABB=ON ENZYME INHIBITORS/CT  
L87 1529 SEA FILE=MEDLINE ABB=ON MOTOR PROTEIN#  
L88 359 SEA FILE=MEDLINE ABB=ON END DIRECT?  
L89 0 SEA FILE=MEDLINE ABB=ON L82 AND (L84 OR L85 OR L86 OR L87 OR L88)

=> fil embase; d que l118

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L109	16	SEA FILE=EMBASE ABB=ON	(THERMOMYCES LANUGINOSUS OR TL) (A) GAMMA
L112	2142	SEA FILE=EMBASE ABB=ON	KINESIN/CT
L113	3476	SEA FILE=EMBASE ABB=ON	MICROTUBULE ASSEMBLY/CT
L114	754	SEA FILE=EMBASE ABB=ON	MICROTUBULE PROTEIN/CT
L115	13611	SEA FILE=EMBASE ABB=ON	MICROTUBULE/CT
L116	316	SEA FILE=EMBASE ABB=ON	END DIRECT?
L117	569	SEA FILE=EMBASE ABB=ON	MOTOR PROTEIN/CT OR MOLECULAR MOTOR/CT
L118	0	SEA FILE=EMBASE ABB=ON	L109 AND (L112 OR L113 OR L114 OR L115 OR L116 OR L117)

=>

=> => fil capl; d que l18

FILE 'CAPLUS' ENTERED AT 12:20:57 ON 05 SEP 2006

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'OBI' IS DEFAULT SEARCH FIELD FOR 'CAPLUS' FILE

L7	1841	SEA	FILE=CAPLUS	ABB=ON	KINESINS/CT
L9	20619	SEA	FILE=CAPLUS	ABB=ON	MICROTUBULE#/OBI
L10	3352	SEA	FILE=CAPLUS	ABB=ON	MOTOR/OBI (L) PROTEIN#/OBI
L15	220	SEA	FILE=CAPLUS	ABB=ON	L7 AND L9 AND L10
L17	48	SEA	FILE=CAPLUS	ABB=ON	END DIRECT?/OBI
L18	3	SEA	FILE=CAPLUS	ABB=ON	L15 AND L17

=> s l18 not l139

L146

3 L18 NOT L139

*previously printed*

=> fil wpix; d que l39; d que l40

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'BI ABEX' IS DEFAULT SEARCH FIELD FOR 'WPIX' FILE

L32 252 SEA FILE=WPIX ABB=ON KINESIN#/BI,ABEX  
L33 811 SEA FILE=WPIX ABB=ON MICROTUBULE#/BI,ABEX OR MICRO TUBULE#/BI,  
ABEX  
L34 120 SEA FILE=WPIX ABB=ON MOTOR PROTEIN#/BI,ABEX  
L35 1863 SEA FILE=WPIX ABB=ON END DIRECT?/BI,ABEX  
L39 3 SEA FILE=WPIX ABB=ON L32 AND L33 AND L34 AND L35

L32 252 SEA FILE=WPIX ABB=ON KINESIN#/BI,ABEX  
L33 811 SEA FILE=WPIX ABB=ON MICROTUBULE#/BI,ABEX OR MICRO TUBULE#/BI,  
ABEX  
L34 120 SEA FILE=WPIX ABB=ON MOTOR PROTEIN#/BI,ABEX  
L35 1863 SEA FILE=WPIX ABB=ON END DIRECT?/BI,ABEX  
L36 4006 SEA FILE=WPIX ABB=ON PROTEIN KINASE#/BI,ABEX  
L37 105 SEA FILE=WPIX ABB=ON L32 AND (L33 OR L34 OR L35)  
L40 1 SEA FILE=WPIX ABB=ON L37 AND L36

=> s l39,l40 not l31

L147 3 (L39 OR L40) NOT (L31) *previously printed*

=> fil DRUGU, JICST-EPLUS, AGRICOLA, PASCAL, CABA, BIOTECHNO, BIOSIS,ESBIOBASE,  
LIFESCI, CONFSCI, DISSABS, JAPIO, ANABSTR, SCISEARCH

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=> d que 175

L64 13861 SEA KINESIN#  
L65 132140 SEA MICROTUBULE# OR MICRO TUBULE#  
L66 7756 SEA MOTOR PROTEIN#  
L67 2654 SEA END DIRECT?  
L75 20 SEA L64 (5A) L65 (5A) L66 (5A) L67

=> s 175 not 168

L148 20 L75 NOT L68

*previously  
printed*

=> fil medl; d que 192

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L85 17967 SEA FILE=MEDLINE ABB=ON MICROTUBULES/CT  
L87 1529 SEA FILE=MEDLINE ABB=ON MOTOR PROTEIN#

L88 359 SEA FILE=MEDLINE ABB=ON END DIRECT?  
L92 9 SEA FILE=MEDLINE ABB=ON L87(8A)L88 AND L84 AND L85

=> s l92 not l83

L149

9 L92 NOT L83

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printed*

=> fil embase; d que l119

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L113 3476 SEA FILE=EMBASE ABB=ON MICROTUBULE ASSEMBLY/CT  
L114 754 SEA FILE=EMBASE ABB=ON MICROTUBULE PROTEIN/CT  
L115 13611 SEA FILE=EMBASE ABB=ON MICROTUBULE/CT  
L116 316 SEA FILE=EMBASE ABB=ON END DIRECT?  
L117 569 SEA FILE=EMBASE ABB=ON MOTOR PROTEIN/CT OR MOLECULAR MOTOR/CT  
  
L119 7 SEA FILE=EMBASE ABB=ON L112 AND (L113 OR L114 OR L115) AND  
L116 AND L117

=> s l119 not l110

L150

7 L119 NOT L110

*previously  
printed*

=> => dup rem l149,l146,l147,l150,l148

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PROCESSING COMPLETED FOR L149

PROCESSING COMPLETED FOR L146

PROCESSING COMPLETED FOR L147

PROCESSING COMPLETED FOR L150

PROCESSING COMPLETED FOR L148

L151 28 DUP REM L149 L146 L147 L150 L148 (14 DUPLICATES REMOVED)

ANSWERS '1-9' FROM FILE MEDLINE

ANSWERS '10-12' FROM FILE CAPLUS

ANSWERS '13-15' FROM FILE WPIX

ANSWERS '16-21' FROM FILE EMBASE

ANSWERS '22-23' FROM FILE BIOTECHNO

ANSWERS '24-27' FROM FILE BIOSIS

ANSWER '28' FROM FILE LIFESCI

=> d iall 1-9; d ibib ed abs hitind 10-12; d iall abeq tech 13-15; d iall 16-28

L151 ANSWER 1 OF 28 MEDLINE on STN DUPLICATE 1  
ACCESSION NUMBER: 2005237850 MEDLINE  
DOCUMENT NUMBER: PubMed ID: 15875026  
TITLE: The bipolar mitotic kinesin Eg5 moves on both microtubules that it crosslinks.  
AUTHOR: Kapitein Lukas C; Peterman Erwin J G; Kwok Benjamin H; Kim Jeffrey H; Kapoor Tarun M; Schmidt Christoph F  
CORPORATE SOURCE: Department of Physics and Astronomy and Laser Centre, Vrije Universiteit, De Boelelaan 1081, 1081 HV Amsterdam, The Netherlands.  
SOURCE: Nature, (2005 May 5) Vol. 435, No. 7038, pp. 114-8.  
Journal code: 0410462. E-ISSN: 1476-4687.  
PUB. COUNTRY: England: United Kingdom  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 200505  
ENTRY DATE: Entered STN: 6 May 2005  
Last Updated on STN: 19 May 2005  
Entered Medline: 18 May 2005

#### ABSTRACT:

During cell division, mitotic spindles are assembled by microtubule-based motor proteins. The bipolar organization of spindles is essential for proper segregation of chromosomes, and requires plus-end-directed homotetrameric motor proteins of the widely conserved kinesin-5 (BimC) family. Hypotheses for bipolar spindle formation include the 'push-pull mitotic muscle' model, in which kinesin-5 and opposing motor proteins act between overlapping microtubules. However, the precise roles of kinesin-5 during this process are unknown. Here we show that the vertebrate kinesin-5 Eg5 drives the sliding of microtubules depending on their relative orientation. We found in controlled in vitro assays that Eg5 has the remarkable capability of simultaneously moving at approximately 20 nm s<sup>-1</sup> towards the plus-ends of each of the two microtubules it crosslinks. For anti-parallel microtubules, this results in relative sliding at approximately 40 nm s<sup>-1</sup>, comparable to spindle pole separation rates in vivo. Furthermore, we found that Eg5 can tether microtubule plus-ends, suggesting an additional

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OM protein - protein search, using sw model

Run on: September 1, 2006, 14:22:02 ; Search time 187.583 Seconds

(without alignments)  
1910.930 Million cell updates/sec

Title: US-09-235-416-1

Sequence: 1 MSGGKIKVVRVPPNARE.....ELRQQAQMEALKTKQER 784

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

A\_Geneseq\_8:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4030	100.0	784	2	AAV06618
2	1684.5	41.8	1714	8	ABM83648
3	1684.5	41.8	1721	8	ABM83647
4	1679	41.7	1199	8	ABM83671
5	1674.5	41.6	1696	8	ABM83653
6	1674.5	41.6	1709	8	ABM83649
7	1674.5	41.6	1722	8	ABM83646
8	1673	41.5	1708	8	ABM83650
9	1669.5	41.4	1699	8	ABM83651
10	1668.5	41.4	1816	3	AAE36227
11	1667.5	41.4	1805	3	ADJ95088
12	1666.5	41.4	1770	6	AAE35317
13	1661.5	41.2	1823	5	ABM87867
14	1660.5	41.2	883	4	AAAM40034
15	1659.5	41.2	1697	8	ABM83652
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17	1658	41.1	1103	6	AAE04316
18	1658	41.1	1103	6	ABG72054
19	1658	41.1	1103	7	ADG63388
20	1635	40.6	1773	4	ABM83908
21	1463.5	36.3	1805	4	ABP68930
22	1431.5	35.5	1362	5	AAU74840
23	1430	35.5	757	4	AAU19569

24	1430	35.5	757	5	ABP51294	ABP51294 Human MDD
25	1423	35.3	762	5	ABG60124	ABG60124 Human DIT
26	1413	35.1	1507	8	ADQ97525	ADQ97525 Human can
27	1412	35.0	1826	7	ADJ69671	ADJ69671 Human hea
28	1412	35.0	1826	8	ADL83235	ADL83235 Human PRO
29	1407.5	34.9	1844	8	ADQ97522	ADQ97522 Mouse can
30	1396.5	34.7	1921	4	ABM82962	ABM82962 Drosophila
31	1386	34.4	1815	8	ADP66952	ADP66952 Human pro
32	1386	34.4	1815	8	ADP66054	ADP66054 Human pro
33	1386	34.4	1815	8	ADP66951	ADP66951 Human pro
34	1386	34.4	1815	8	ADP66053	ADP66053 Human pro
35	1347	33.4	944	7	ADM04401	ADM04401 Human pro
36	1347	33.4	944	9	AEC87331	AEC87331 Human CDN
37	1347	33.4	1317	9	AED07567	AED07567 Chromosom
38	1347	33.4	1392	6	AAE32129	AAE32129 Human cyt
39	1347	33.4	1392	7	ADJ94858	ADJ94858 Novel NOV
40	1347	33.4	1393	8	ADN00367	ADN00367 Novel hum
41	1311.5	32.5	1375	5	ABM79531	ABM79531 Human kin
42	1311.5	32.5	1375	5	ABM84481	ABM84481 Human kin
43	1311.5	32.5	1375	5	AAE22525	AAE22525 Human HSK
44	1307	32.4	1394	7	ADJ94856	ADJ94856 Novel NOV
45	1278.5	31.7	504	3	ABM63189	ABM63189 Gene 5 hu

#### ALIGNMENTS

RESULT 1  
ID AAV06618 standard; protein; 784 AA.  
XX  
AC AAV06618;  
DT 26-OCT-1999 (first entry)  
XX  
DE Thermomyces lanuginosus kinesin motor protein TL-gamma.  
XX  
XX TL-gamma; kinesin; motor protein; microtubule; unc-104; infection;  
KM neurodegenerative disease; Alzheimer's disease; Parkinson's disease;  
KW Huntington's disease; amyotrophic lateral sclerosis.  
XX  
OS Thermomyces lanuginosus.  
XX  
PN WO9337659-A1.  
PD 29-JUL-1999.  
XX  
PF 22-JAN-1999; 99WO-US001355.  
XX  
PR 23-JAN-1998; 98US-0072361P.  
XX  
(REGC) UNIV CALIFORNIA.  
XX  
Sakowicz R, Goldstein LSB;  
WPI; 1999-493950/41.  
N-PSDB; AAX87656.  
XX  
New nucleic acid encoding microtubule motor protein, used for diagnosis  
of fungal infection and neurodegenerative disease.  
XX  
PS Claim 5; Page 70-71; 75pp; English.  
XX  
This sequence represents Thermomyces lanuginosus TL-gamma, a novel ATP-  
dependent, plus end-directed microtubule motor protein that is a member  
of the unc-104 family and kinesin superfamily. The invention provides TL-  
gamma nucleic acids (see AAX87656), proteins and antibodies, and methods  
of screening for TL-gamma modulators potentially useful for treating  
hypothal fungal infections and diseases caused by mutated TL-gamma, e.g.  
neurodegeneration involving anterograde axonal transport, such as  
Alzheimer's, Parkinson's or Huntington's diseases or amyotrophic lateral  
sclerosis. Detection of TL-gamma allows differentiation between hypothal  
and non-hypothal fungal infections

```

XX      SQ      Sequence 784 AA;
Query Match      100.0%; Score 4030; DB 2; Length 784;
Best Local Similarity 100.0%; Pred. No. 6.5e-299;
Matches 784; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MSGGNIKVYVVRPPNAREIDRGACIYRMESGNOTILTPPGAEBKARKSGKTTIDGPK 60
DB      1  MSGGNIKVYVVRPPNAREIDRGACIYRMESGNOTILTPPGAEBKARKSGKTTIDGPK 60
QY      61  AFAFPRSYSPFKNAPNARYROEDLFODLGVPLLDNAFKGNNNCIFAYGOTSGSKSYMMG 120
DB      61  AFAFPRSYSPFKNAPNARYROEDLFODLGVPLLDNAFKGNNNCIFAYGOTSGSKSYMMG 120
QY      121 YGKEHGVIPRICODMERRIINELQDKNLTCTVEVSYLEIYNERVRDLNLPSTKGNLKVE 180
DB      121 YGKEHGVIPRICODMERRIINELQDKNLTCTVEVSYLEIYNERVRDLNLPSTKGNLKVE 180
QY      181 HPSGTPIYVEDLAKLVYRSFOEIEINLMDENGNKARTVAATNMNETSSRSHAVFTLTQKH 240
DB      181 HPSGTPIYVEDLAKLVYRSFOEIEINLMDENGNKARTVAATNMNETSSRSHAVFTLTQKH 240
QY      241 DEETKMDTEKVAKISLVDLAGEBRATSTGATGARLKEGAENRSSTLGRVIALADMS 300
DB      241 DEETKMDTEKVAKISLVDLAGEBRATSTGATGARLKEGAENRSSTLGRVIALADMS 300
QY      301 GKQKNQVLPRYDSVLTWLLKDSLGNSMTAMIAISPADINEETLTSLRYADSAKRIL 360
DB      301 GKQKNQVLPRYDSVLTWLLKDSLGNSMTAMIAISPADINEETLTSLRYADSAKRIL 360
QY      361 NNAVNNEDNANMIRELKEELAQLRSKLQSSGGGGGAGSGGSPVEESTPPDPLEKOY 420
DB      361 NNAVNNEDNANMIRELKEELAQLRSKLQSSGGGGGAGSGGSPVEESTPPDPLEKOY 420
QY      421 SIOOPDATYKMSKKEIVEQLNQSEKLYRDLNQTEWEKLAKEEIHKEEALAEIGISI 480
DB      421 SIOOPDATYKMSKKEIVEQLNQSEKLYRDLNQTEWEKLAKEEIHKEEALAEIGISI 480
QY      481 EKGFGVPYHKSMPHLVNSDDPLAECLVYNIKKPQTRVGNVNOTQAEIRLNGSKILK 540
DB      481 EKGFGVPYHKSMPHLVNSDDPLAECLVYNIKKPQTRVGNVNOTQAEIRLNGSKILK 540
QY      541 EHCTEENVNVVTIYNEKAAVWVNGVRIDKPTRLSGRIIIGDPHIFRPNHPEBARAE 600
DB      541 EHCTEENVNVVTIYNEKAAVWVNGVRIDKPTRLSGRIIIGDPHIFRPNHPEBARAE 600
QY      601 ROEQSLLRHSVTNSQLGSPAPGRHDTLSKAGSDADGDSRSDSPPLPHFRGKSDMFWYAR 660
DB      601 ROEQSLLRHSVTNSQLGSPAPGRHDTLSKAGSDADGDSRSDSPPLPHFRGKSDMFWYAR 660
QY      661 EASASAILGIDOKISHLTDELALPDVQKARAVRGLVEDNEDSSOSSFFPRDKYMSN 720
DB      661 EASASAILGIDOKISHLTDELALPDVQKARAVRGLVEDNEDSSOSSFFPRDKYMSN 720
QY      721 GTINDFSLPTATITMPTPRSDDDGDALFFGDGKSKODASNVNVEEELRQOQAQWESALKTA 780
DB      721 GTINDFSLPTATITMPTPRSDDDGDALFFGDGKSKODASNVNVEEELRQOQAQWESALKTA 780
QY      781 KOEF 784
DB      781 KOEF 784

```

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XX      XX      gene therapy; human diagnostic and therapeutic polynucleotide; dthp.
XX      OS      Homo sapiens.
XX      PN      WO2004023973-A2.
XX      PD      25-MAR-2004.
XX      PF      12-SEP-2003; 2003WO-US028227.
XX      PR      12-SEP-2002; 2002US-0410259P.
XX      PR      12-SEP-2002; 2002US-0410260P.
XX      PA      (INCY-) INCYTE CORP.
XX      PI      Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,
PI      Harshborne RA, Suchorolski MT, Altus CM, Plets SJ, Elder LV,
PI      Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP,
PI      Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH,
PI      Peralta CH, Anderson SB, Rioux P, Shen ED, Wu MC, Scuve LL,
PI      Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kilton ES,
PI      Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D,
PI      Patury S, Shi X, Suarez CJ;
XX      DR      WPI: 2004-329368/30.
XX      DR      N-PsDB: ACN42300.
XX      PT      New diagnostic and therapeutic polynucleotides and polypeptides, useful
XX      PT      in diagnosing a condition, disease or disorder associated with human
XX      PT      molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
XX      PS      in gene mapping.
XX      PS      Claim 27; Page: 190pp; English.
XX      CC      The invention relates to novel diagnostic and therapeutic polynucleotides
XX      CC      selected from one of the 2722 sequences defined in the specification. A
XX      CC      polynucleotide of the invention may have a use in gene therapy. The human
XX      CC      diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be
XX      CC      used to diagnose a particular condition, disease or disorder associated
XX      CC      with human molecules, e.g. cell proliferative disorders,
XX      CC      autoimmune/inflammatory disorder, developmental disorder, endocrine
XX      CC      disorder, neurological disorders, gastrointestinal disorders, or
XX      CC      infections caused by virus, bacteria, fungi or parasite. The dthp
XX      CC      molecules may also be used in genetic mapping, in identifying individuals
XX      CC      from minute biological samples, in detecting single nucleotide
XX      CC      polymorphisms, as molecular weight markers, and for somatic or germline
XX      CC      gene therapy. The present sequence represents a dthp protein of the
XX      CC      invention. Note: The sequence data for this patent is not represented in
XX      CC      the printed specification, but was obtained in electronic format directly
XX      CC      from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX      SQ      Sequence 1714 AA;
Query Match      41.8%; Score 1684.5; DB 8; Length 1714;
Best Local Similarity 46.5%; Pred. No. 6.4e-119;
Matches 358; Conservative 127; Mismatches 174; Indels 111; Gaps 16;

QY      4  GGNITVYVVRPPNAREIDRGACIYRMESGNOTILTPPGAEBKARKSGKTTIDGPKA 63
DB      3  GASVYVAVVRPPNAREIDRGACIYRMESGNOTILTPPGAEBKARKSGKTTIDGPKET 51
QY      64  PDRSYWSPDKNAP---NYARQEDLFODLGVPLLDNAFKGNNNCIFAYGOTSGSKSYMMG 120
DB      52  FDYSTWS--HTSPEDINAYSQQVYRDIGEBNLAHAFGYVNCIFAYQOTGAGSYTMMG 109
QY      121 YGK--EHGVIPRICODMERRIINELQDKNLTCTVEVSYLEIYNERVRDLNLPSTKGNLK 178
DB      110  KOEKDQGGIIPQLGDLFSRLNDTTND--NMGYSVSVSMETICEVRDLNLPKNGNLRY 168
QY      179  REHPSGTPIYVEDLAKLVYRSFOEIEINLMDENGNKARTVAATNMNETSSRSHAVFTLTQK 238
DB      169  REHPLGLGYVEDLSKLAVTSYNDIODLMDSGNKARTVAATNMNETSSRSHAVFTLTQK 228

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QY 239 WHDETMDTEKAKISLVLDLASERATSTGATGARTLKEGAEINRSSTLGRVIALADW 298
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 229 RHDAETNITTEKYSKISLVLDLASERADSTGAKGTRKEGANINKSLTTIGKVISALAEW 288
QY 299 SSG-----KOKNOQVYPRDSVLTWLLKDSLGSNSMTAMIAISPADINFEETLSTLRYA 353
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 289 DSGNKNKKKKKTDFIPYRDSVLTWLLRENLGNSRTAMVAALSPADINDETSTLRYA 348
QY 354 DSAKRITKNAHVNNEDPNAARMIRELKEELAQRLSKLSSGGGG-----CGAG----- 399
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 349 DRAKQIRCNAINVEDPNNKILRELKDEVTLRDLVLAQGLDITDNTVPGPKYVSLE 408
QY 400 -----GSGGPVEESYPDPTEPLEKOIVSIQOPDATVKKMS-----KAEI 437
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 409 NNNLNKGCTVNEAPDPLSTVTNALVGM-SPSSSLALSSRAASVSLHERILFAPGSEEA 467
QY 438 VEOLNQSEKLYRDNLQNTWEKLAETIEIKEREALAEGLISIEK--GFGVPHSKEMPH 495
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 468 IERLKETEKIILAEINETWEKELRTEAIRMERELALAEKVAMRREDGTLGVSPKKTPH 527
QY 496 LVNLSDDPLAECLVYNIKPGQTRVGNVNDTQAEIRLNSKILKEHCTEN-----VDN 550
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 528 LVNLEBDPLMSECLLYIKGQITRVGEXDERQDIVLSGHFIKEHCVRSDSRGSGSEA 587
QY 551 VVTIVPEKAAVWVNGVRIDKPTRLRSYRIILGDFHIFRFNHPPEARARQEQSLRRHS 610
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 588 VVTLPECGADTVYNGKKTPEPILRSQNLIIIMKSHVFFNHPQARQERER----- 640
QY 611 VTNLSQSGPAPGRHDTLRKAGSDADGSDRSPLPHFRKQSDWFYARREASAILGLD 670
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 641 -----TPCAETPAEPVDMAPQAQELLLEK-QGID 667
QY 671 QKISHLTDELDALFDVDQKARAVRGVLVEDNEDSDSSGSPVRDKMSN 720
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 668 MK--QEMORQLQLELDQYRREDEATYLL-QQRLDESLEALQKQMS 714

RESULT 3
ABM83647
ID ABM83647 standard; protein: 1721 AA.
XX
AC ABM83647;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3896.
XX
KM gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
XX
PI 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Hartshorne TA, Suchorolski MT, Altue CM, Pites SJ, Elder LV;
PI Mooney BM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Steaney KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vicit UA, Kitton ES;
PI Xu Y, Kwong W, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Fatuny S, Shi X, Suarez CJ;
XX
MPI; 2004-329368/30.

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DR N-PSDB; ACN42299.
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 27; Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders.
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPD at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 1721 AA;
Query Match 41.8%; Score 1684.5; DB 8; Length 1721;
Best Local Similarity 46.5%; Pred. No. 6,5e-119;
Matches 358; Conservative 127; Mismatches 174; Indels 111; Gaps 16;
QY 4 GGNIVVVRPRPNAREIDRGAKCIRVMGNOILPPPAEKAKKSGKTINDGKAPFA 63
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 GASVKAIVRRVPRNSREMSKCIILQMSGSTTVINPQPKET-----PKSFS 51
QY 64 FDRSYSPDKNAP---NYARQEDLPQDLGVPLDIAFAKGNNCIFAYGQSGSKSYSMG 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 52 FDSYMS--HTSPEDINVASQKQVYRDIGEBMLQHAPEGNVICIFAYGQGAAGKSTYMG 109
QY 121 YGK-EHGVIPRIQDMPFRINELQKQKLTCTVEVSYLEIYNERVADLLPSTKGLKV 178
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 110 KQEKQGGIIPQCEBDFSRINDTND-NMYSVEVSWEIYCEVRDILLPNKNGLRV 168
QY 179 REHPSTGPYVEDAKLVASFOEINLMDENKAKARVAATNNNETSSRSAAVTLTLTK 228
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 169 REHPPLGPIYVEDLSKLVTSYNDIODLMSGNKARTVAATNNNETSSRSAAVENIIFTK 228
QY 239 WHDETMDTEKAKISLVLDLASERATSTGATGARTLKEGAEINRSSTLGRVIALADW 298
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 229 RHDAETNITTEKYSKISLVLDLASERADSTGAKGTRKEGANINKSLTTIGKVISALAEW 288
QY 299 SSG-----KOKNOQVYPRDSVLTWLLKDSLGSNSMTAMIAISPADINFEETLSTLRYA 353
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 289 DSGNKNKKKKKTDFIPYRDSVLTWLLRENLGNSRTAMVAALSPADINDETSTLRYA 348
QY 354 DSAKRITKNAHVNNEDPNAARMIRELKEELAQRLSKLSSGGGG-----CGAG----- 399
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 349 DRAKQIRCNAINVEDPNNKILRELKDEVTLRDLVLAQGLDITDNTVPGPKYVSLE 408
QY 400 -----GSGGPVEESYPDPTEPLEKOIVSIQOPDATVKKMS-----KAEI 437
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 409 NNNLNKGCTVNEAPDPLSTVTNALVGM-SPSSSLALSSRAASVSLHERILFAPGSEEA 467
QY 438 VEOLNQSEKLYRDNLQNTWEKLAETIEIKEREALAEGLISIEK--GFGVPHSKEMPH 495
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 468 IERLKETEKIILAEINETWEKELRTEAIRMERELALAEKVAMRREDGTLGVSPKKTPH 527
QY 496 LVNLSDDPLAECLVYNIKPGQTRVGNVNDTQAEIRLNSKILKEHCTEN-----VDN 550
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 528 LVNLEBDPLMSECLLYIKGQITRVGEXDERQDIVLSGHFIKEHCVRSDSRGSGSEA 587
QY 551 VVTIVPEKAAVWVNGVRIDKPTRLRSYRIILGDFHIFRFNHPPEARARQEQSLRRHS 610

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Db 588 VVTLPECEGADTYVNGKVTBPSILRSGNRITIMGKSHVFRFNNPEQARQERER----- 640  
Qy 611 VVNSQLGSGAPRGRHRTLSKAGSDADGDSRSDSPLEPHFGKOSDMFYARREASALIGD 670  
Db 641 -----TPCAETPAEPVDMAFAQRELLER-OGID 667  
Qy 671 OKISHLTDELDELFPDVOKARAVRGGLVEDNEDSDSGSPFVRDKYMN 720  
Db 668 MK--QEMBRLOLEBDYRREBEATYLE-QQRLDYSEKLEMLQKQMS 714

## RESULT 4

ABM83671

ID ABM83671 standard; protein; 1199 AA.

AC ABM83671;

DT 18-NOV-2004 (first entry)

DE Human diagnostic and therapeutic protein SEQ ID NO:3920.

KM gene therapy; human diagnostic and therapeutic polynucleotide; dthp.

OS Homo sapiens.

PN MO2004023973-A2.

PD 25-MAR-2004.

PF 12-SEP-2003; 2003WO-US028227.

PR 12-SEP-2002; 2002US-0410259P.

PR 12-SEP-2002; 2002US-0410260P.

(INCY-) INCYTE CORP.

PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;

PI Harchshore TR, Suchorolski MT, Altus CM, Plets SJ, Elder LV;

PI Mooney EM, Deleagane AM, Panesar IS, Banville SC, Reddy TP;

PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Geretin EH;

PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;

PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Klinton ES;

PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;

PI Patury S, Shi X, Suarez CJ;

XX WPI: 2004-329368/30.

DR N-PSDB; ACN42323.

XX New diagnostic and therapeutic polynucleotides and polypeptides, useful

PT in diagnosing a condition, disease or disorder associated with human

PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or

PT in gene mapping.

XX Claim 27; Page: 190pp; English.

PS The invention relates to novel diagnostic and therapeutic polynucleotides

CC selected from one of the 2722 sequences defined in the specification. A

CC polynucleotide of the invention may have a use in gene therapy. The human

CC diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be

CC used to diagnose a particular condition, disease or disorder associated

CC with human molecules, e.g. cell proliferative disorders,

CC autoimmune/inflammatory disorder, developmental disorders, endocrine

CC disorder, neurological disorders, gastrointestinal disorders, or

CC infections caused by virus, bacteria, fungi or parasite. The dthp

CC molecules may also be used in genetic mapping, in identifying individuals

CC from minute biological samples, in detecting single nucleotide

CC polymorphisms, as molecular weight markers, and for somatic or germline

CC gene therapy. The present sequence represents a dthp protein of the

CC invention. Note: The sequence data for this patent is not represented in

CC the printed specification, but was obtained in electronic format directly

CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

CC

XX

SQ Sequence 1199 AA;

Query Match 41.7%; Score 1679; DB 8; Length 1199;

Best Local Similarity 41.8%; Pred. No. 9,8e-119;

Matches 385; Conservative 139; Mismatches 232; Indels 164; Gaps 21;

Qy 4 GGNIKVVRVRPPFNAREIDRGAKCIVRMEGNOTILTPPGAEEKARKSGKTIMDGPFA 63

Db 3 GASVAVAVRVPFRNRETSKESKCIQMOGNSTSIINKNPE-----APKFS 51

Qy 64 PDRSYMSF-DKNAFYARQEDLPQDLYPLDPAFKGNVICFAAGTSGSKSYSMGYG 122

Db 52 FDYSYMSHTSPEDPCFASQNRVYNDIGKEMLLHAEGYNVICFAAGTSGASYTMKQ 111

Qy 123 KEH--GVTPICQDMFRRIINELQDKNLTCTVEVSELYEIVNERVVDLNPSTKGLKRE 180

Db 112 EESQNGIIFQICEELFEKIND-NCNEMSYSEVSYMTIICERVVDLNPKNKGLRARE 170

Qy 181 HPSTGPVVEDLAKLVVRSFOEIEMLDEGNKARTVAATNMNETSRSRAVFTLTQKMH 240

Db 171 HPLGIPYEDLSKLAVTSTYDIADLMDAGNKARTVAATNMNETSRSRAVFTLTQKMH 230

Qy 241 DEETKMDTEKAKISLVPLAGSERATSGATGARLKEGAEINRSUSTGRYIADLADN-- 298

Db 231 DNETMLSTEBKSKISLVPLAGSERADSTGAGTRLKEGANINKSLTTLGKVISALAEVDN 290

Qy 299 ---SSGKKKKQQLVPRDSVLTWLLKDSLGGNSMTAMTAAISPADINFEETSLTRYADS 355

Db 291 CTSKSKKKKKKTDFIYRDSVLTWLRNLDGNSRTAMVAAISPADINDELSTLRVADR 350

Qy 356 AKRIKNAHVNEDPNAFMIRELKEBLAQRSLKSGSGG-----GGAG----- 399

Db 351 AKQIKNAVINEDPNAKVLRELKEVTRLKDLRQGLGDIIDPLIDYSGSGSKYLK 410

Qy 400 -----GSGPVESEYPPDPTLEKQ-----IVSTQPPATYKK 431

Db 411 DFQNNKRRYLLASENQRGHFSTASMGSLTSS-PSSCSLSQVGLTSTVSIQ-ERINST 467

Qy 432 MSKAIIVLNQSEKLYVDLNOTWEKLAETEEIHKEREALAELEGISIEK--GEVGPYH 489

Db 468 PGGEAIRELKESEKILNELNETWEKRLKTEALIMEBELLAEAGVAILREGGLGVFS 527

Qy 490 SKEMPHLVNLSDDPLLAECGLVYNIKPGQTRVGNVQDQAEIRLNGSKILKEHCTFENV- 548

Db 528 PKKTPHLVNLNEDPLMSECLLYYIKDGIYRQGADEBRQDVIIVLSGAHKEHCIFRSE 587

Qy 549 ----DNVTIYVNEKAAMNNGVRIDKPTRLRSGYRIILGDFHFRFNNPEARER--- 601

Db 588 SNSGEIVTLPECSERSETYVNGKRVSPVQLRSGNRITIMGKSHVFRFNNPEQARERKT 647

Qy 602 -----QEOSLRLHSVTNSQ-----LGSAPAGHDBRTLKAGSDA 635

Db 648 PSAETPSEPVDWTFPAQRELLERKQIDMKQEMEKRLQEMEILYKKEKEADLLLEQRIDA 707

Qy 636 DGDSDSDS-----PLPHFR 649

Db 708 DSDSDSDSDKSCSESWKLITSLREKLPPSKLQITVKKCGLPSSGKKEPIKMYQIPQR 767

Qy 650 --GKSDPFYARREASAILGLDKISHLTP-----DELALFPDVOKARAVRGGLVEDN 702

Db 768 RLKSKSKVWTISDLKIQVKEICYEVA-LNDFRRSRQIEALIVKMLCAMYGGKQPN 826

Qy 703 EDDSDSGSPVADKYSNGTIDNFSLPDPAITMPGTPRSD-----DGDALFFGDKSKXOD 757

Db 827 E-RDSWRAY-ARDVMDTGVGVDEKEDVMAIGKSGSTVDVLDKMHDKEDLIGVKKQNN 884

Qy 768 ASNVDEBLRQQAQMEAL 777

Db 885 MKDEIKVILRNMLMEKVL 904

## RESULT 5

ABM83653



ID AEM3653standard; protein; 1696 AA.  
 AC AEM3653;  
 DT 18-NOV-2004 (first entry)  
 XX  
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:3902.  
 XX  
 KW gene therapy; human diagnostic and therapeutic polynucleotide; dthp.  
 XX  
 OS Homo sapiens.  
 PN WO2004023973-A2.  
 PD 25-MAR-2004.  
 XX  
 PF 12-SEP-2003; 2003WO-US028227.  
 XX  
 PR 12-SEP-2002; 2002US-0410259P.  
 XX  
 PR 12-SEP-2002; 2002US-0410260P.  
 XX  
 RA (INCY-) INCYTE CORP.  
 XX  
 PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;  
 PI Hartschorne TP, Suchorolski MT, Altus CM, Plets SJ, Elder LV;  
 PI Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy RP;  
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;  
 PI Peraltia CH, Anderson SE, Rioux P, Shen EJ, Wu MC, Stuve LJ;  
 PI Lagace RE, Spito PA, Stewart EA, Wingrove J, Valt UA, Kilton ES;  
 PI Xu Y, Kwong M, Policky JT, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;  
 PI Patery S, Shi X, Suarez CJ;  
 XX  
 DR MPI: 2004-329368/30.  
 DR N-PSDB; ACN42305.  
 XX  
 PT New diagnostic and therapeutic polynucleotides and polypeptides, useful  
 PT in diagnosing a condition, disease or disorder associated with human  
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
 PT in gene mapping.  
 XX  
 PS Claim 27; Page; 190pp; English.  
 XX  
 XX The invention relates to novel diagnostic and therapeutic polynucleotides  
 CC selected from one of the 2722 sequences defined in the specification. A  
 CC polynucleotide of the invention may have a use in gene therapy. The human  
 CC diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be  
 CC used to diagnose a particular condition, disease or disorder associated  
 CC with human molecules, e.g. cell proliferative disorders,  
 CC autoimmune/inflammatory disorders, developmental disorders, endocrine  
 CC disorder, neurological disorders, gastrointestinal disorders, or  
 CC infections caused by virus, bacteria, fungi or parasite. The dthp  
 CC molecules may also be used in genetic mapping, in identifying individuals  
 CC from minute biological samples, in detecting single nucleotide  
 CC polymorphisms, as molecular weight markers, and for somatic or germ-line  
 CC gene therapy. The present sequence represents a dthp protein of the  
 CC invention. Note: The sequence data for this patent is not represented in  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)  
 XX  
 XX Sequence 1696 AA;  
 XX

```

Query Match      41.6%  Score 1674.5; DB 8; Length 1666;
Best Local Similarity 46.4%; Pred. No. 3.7e-118;
Matches 356; Conservative 128; Mismatches 175; Indels 109; Gaps 16

QY      4  GGNIRVVVRVPPFAREIDRGAKCIVRNEGNQITLTPPGAEKARKSGKTMIDPKAPA 63
      ||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db       3  GASVYVAVRVPPFNSREMSRDSKCTIQMSGSTTIVNKPQKPYT-----PKSFS 51

QY      64  FDRSYWSPDKNAP---NYARQEDLFQDGVPLDIAFGYNNCCFAYGOTSGKSYSMWG 120
      |||||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db       52  FDIYSYMS--HRSPEIDINYSQKQVRKRDIGEMLQAHAFGYNVCIPIAYGOTGKGSYTMWG 109

```

QY	121	YGK--EHEVPIPCODMFRINELQDKDLCTGVESYLEIYNERRDILNPTKCNLKY	178
Db	110	KOEKQOQGIIPQCDLFSRLINDTND--MMSVVEVSWEIICYERDILNPKCNLRV	168
QY	179	REHPTGCVYVEDLAKLVVRSFOEINLMDGKKAFTVAATNNMETSSRSHAVTTLTLTK	238
Db	169	REHPLTGGYVEDLSKLAATVSNDIDQIMDSGNKARTVAATNNNETSSRSHAVNNITFTQK	228
QY	239	WHDESTKQDTEKVAKISLVLDAGSERATSTGATGARLKEGAEINRSLSTLGRVIALADM	298
Db	229	RHDAETNITTEKVSKISLVLDAGSERADSTGAKTRLKEGANINKSLTTLGKVISALAEW	288
QY	229	---SSGRKQKQVLVYRDSVLTWLLKDSLGSNSMTAMLAISPADNFEETLSTLRYADS	355
Db	289	XPPOKAKKKKKTDFIPYRDSVLTWLLRENLGNSRTAMVAALSPADINYEETLSTLRYADR	348
QY	356	AKRINHAHVVEDPAPARIMRELKEELAOLRSLTQSSGGG-----GGAG-----	399
Db	349	AKQIRCNAINVEDPPNNKILRELKDEVTRRLDLYAOGGLDITDTNTVPGGPKVSDLENN	408
QY	400	--GSGRPVEESYPDPPLPKQIVSIQOPDATVKKMS-----KAEIYE	439
Db	409	NLNRGTVNEAPDPLSTVTNMLVGM-SPSSLSALSSRAVSLSHERILFAPGSEATE	467
QY	440	QLNQGSEKLYRDLNQCWEKLAETIEHKEREALABELGISIEK--GFVGRPHSKEMPHLY	497
Db	468	RLKETEKIIAEINTEWEEKLRRTETRIEMERELLLBEMGAMREDDGTLVFPSPKTPHLV	527
QY	498	NLSDPPLAECLVNYIKPGOTFRVGVANNODTOAEIFLNSGKLKEHCFEN-----VDNVY	552
Db	528	NLNEEDPLMSECLYITKQGITRVGRDEGERRDDIVLSGHFIKEEHCVFRSDRSGSEAYV	587
QY	553	TIVPEKAAVWVNGVRIIDKPTRLRSQGYRIILGDFAHIFRHNPEEARAEBOQSLNHSYV	612
Db	588	TLPECEGADTYVNGKKTVEPSILRSGNRIIMGKSHVFRNHPEQARQERER-----	638
QY	613	NSQLGSPAPGHHDRITLSAAGSDADGSDSDSFLPHFRGKDSQWFFARREPAASAILGLDK	672
Db	639	-----TPCAETPAPVPMVMAFAQRELLEK-QGIDMK	667
QY	673	ISHLTDELDELFPDVKARAVRGLVEDNEEDSDSSSPFVADKXMSN	720
Db	668	--QEWQRLOLELDDOYRRREBEATYLLR-QQRLDYESKLEALQKQWDS	712
RESULT 6			
ABM83649			
ID	ABM83649	standard; protein; 1709 AA.	
XX	ABM83649;		
AC			
XX			
DT	18-NOV-2004	(first entry)	
XX			
DE	Human diagnostic and therapeutic pprotein SEQ ID NO:3898.		
XX			
KW	gene therapy; human diagnostic and therapeutic polynucleotide; dltnc.		
XX	Homo sapiens.		
OS			
XX	MO2004023973-A2.		
FN			
PD	25-MAR-2004.		
PF	12-SEP-2003; 2003WO-US028227.		
XX			
PR	12-SEP-2002; 2002US-0410259P.		
XX	12-SEP-2002; 2002US-0410260P.		
XX			
PA	(INCY-) INCYTE CORP.		
XX			
PI	Schmidt JP, Wright RJ, Bruns CM, Marianovic MM, Shen F;		
PI	Hatchborne TA, Suchorolski MT, Altus CM, Plets SJ, Elder LV;		
PI	Mooney EM, Deleane AM, Panesaris, Banville SC, Reddy TP;		

PD 25-MAR-2004 .  
XX 12-SEP-2003; 2003WO-US028227 .  
PF  
XX 12-SEP-2002; 2002US-0410259P .  
PR 12-SEP-2002; 2002US-0410259P .  
PR 12-SEP-2002; 2002US-0410260P .  
XX  
XX (INCY-) INCYTE CORP .  
XX  
XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;  
PI Hartschornie TA, Suchorolski MT, Altus CM, Fltcs SJ, Elder LV;  
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;

PI Steven KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gershin EH;  
PI Perleita CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve IL;  
PI Lagace RE, Spiro PA, Stewart EA, Wingofove J, Vilt UA, Kitton ES,  
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D,  
PI Patuary S, Shi X, Saez CJ;  
XX MPI: 2004-329368/30.  
DR N-PSDB; ACN42301.  
XX  
XX  
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful  
XX in diagnosing a condition, disease or disorder associated with human  
XX molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
XX in gene mapping.  
XX  
XX  
XX Claim 27; Page: 190pp; English.  
XX  
XX The invention relates to novel diagnostic and therapeutic polynucleotides  
XX selected from one of the 2722 sequences defined in the specification. A  
XX polynucleotide of the invention may have a use in gene therapy. The human  
XX diagnostic and therapeutic polynucleotides (ditnp) or polypeptides may be  
XX used to diagnose a particular condition, disease or disorder associated  
XX with human molecules, e.g. cell proliferative disorders,  
XX autoimmune/inflammatory disorder, developmental disorder, endocrine  
XX disorder, neurological disorder, gastrointestinal disorders, or  
XX infections caused by virus, bacteria, fungi or parasite. The ditnp  
XX molecules may also be used in genetic mapping, in identifying individuals  
XX from minute biological samples, in detecting single nucleotide  
XX polymorphisms, as molecular weight markers, and for somatic or germline  
XX gene therapy. The present sequence represents a ditnp protein of the  
XX invention. Note: The sequence data for this patent is not represented in  
XX the printed specification, but was obtained in electronic format directly  
XX from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)  
XX  
XX Sequence 1709 AA;  
SQ

Query Match	41.6%	Score 1674.5	DB 8	Length 1709
Best Local Similarity	46.4%	Pred. No. 3.7e-118		
Matches 356	Conservative 128	Mismatches 175	Indels 109	Gaps 16

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QY      4 GGNIKVWVRVPNNARIEDRGAKCIYRMGNOJITLTPPGAEBAEKARKSGKTIWDGPKARA 63
Db      3 GASVKAARVRPFNSHEMRSDSKCIIOMSGSTTTTINVPKOPKET-----FKPS 51
QY      64 PDRSYWSPDKNP---NYAROEDLPDOLGVPLLDNAPFKGNNNICIFAYGGOTGSKSXMMG 120
Db      52 FPIYSWVS--HTSPEDINVASOKOYVDIGEBMIOHAFEGYNVICIFAYCGOTGAASKSTMMG 109
QY      121 YGK--EHGVIPIICODMPFRINELOKKULJTCTVEVSYLEIYNERVDDLNPSTKGNLKY 178
Db      110 KQEKDOQGIIIPQLCEBTLFSRINDTTND-NMSYSVEVSYPEICYERVDLLNPNKNGLNRV 168
QY      179 RHPSTGPVVEDLAKLVARSFOEINLEMBGNKARVAATNMNETSSRSNAVTLLLTOK 238
Db      169 RHPLPLGPVVEDLSKIATVTSYNDIOQLMOBSGNARVAATNMNETSSRSNAVTNIITFK 228
QY      239 WHDEETKMOTEEKAKISLYDLAGESEPATSGATGATLKGEAEINRSISTAGRYAIALADM 298
Db      229 RHDAETNITTEKYSKISLYDLAGESEADGTGACGTRILKGCANINKSLTTLGKYSISLAEN 288
QY      299 ---SSGKKQKNOLVPIRDSVLTWLTKDSLJGNSMTAMIAAISPADINFEEETSLTRYADS 355
Db      289 XPRQWKKKKKTFPIPRYDSVLTWLIRENJGNSRTMVAAISPADINYDETTSLTRYADR 348
QY      356 AKRIKSHAVVNDDPNAARMIRELKEELAOLRSKLQSSGGGG-----GGAG----- 399
Db      349 AKOIICNMAVINBPNNKILRELDEVTRLRDLLYAAGLGDTIDTNVTPGGPKVYSLLENN 408
QY      400 --GSGGPVEESYPDPDPLEKQIVSIOOPATAVKMS-----KAIVE 439
Db      409 NLNRGGTVNEARDPLSTVNALVGM-SPSSLSALSRAASVSLHERILLFAPGSEBALE 467
QY      440 QLNQSEKLRJDNLQNTWEELKATTEETHKEREALBELGISIEK--GFVGPHYSKEMPHLY 497
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Db 468 RLKTEKIKIAELNFTWEEKLRTETAIRMERELLALMEGVAMREDGGTLGVFSFKTPHLV 527  
 Qy 468 NLSDPLLAECVLVNIKQGFIVGVVNDQTOAELFNLGSKILKEHCTFEN-----VDNVY 552  
 Db 528 NLNEDPLMSECLLYIKGITRVRGDEGDERRODIVLSGFHFIKEEHCFVFSRSGSEAVV 587  
 Qy 553 TIVPEKKAVMVNGVRIDKPTRLRSGYRIILGDPHIFRPNHPEAPAEKROEQSLRHSTV 612  
 Db 568 TLEPEGADTYVNGKAVTEPSTLRSGNRIIMGKSHVFRNHPQARQEKER-----638  
 Qy 613 NSQLGSPAPGRHRTLSKAGSDADGDSRSDSLPHFRGKDSDFYARREAAAIIGLDOK 672  
 Db 639 -----TCAETPAPVPDWMFAQRELLER-QGIDMK 667  
 Qy 673 ISHLTDELDALEFDVQKARAVRGLVEDNEDSDSSSPVADKYSN 720  
 Db 668 --QEWEORLQELDEDQYRREREATYILE-QGRLDYESKLEALQKQMS 712  
 RESULT 7  
 ABM83646  
 ID ABM83646 standard; protein, 1722 AA.  
 XX ABM83646;  
 AC  
 XX  
 DT 18-NOV-2004 (first entry)  
 DE Human diagnostic and therapeutic pproteIn SEQ ID NO:3895.  
 XX gene therapy; human diagnostic and therapeutic polynucleotide; dithp.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO2004023973-A2.  
 PN  
 XX  
 PD 25-MAR-2004.  
 XX  
 XX 12-SEP-2003; 2003WO-US028227.  
 PF  
 XX  
 PR 12-SEP-2002; 2002US-0410259P.  
 PR 12-SEP-2002; 2002US-0410260P.  
 XX  
 PA (INCY-) INCYTE CORP.  
 XX  
 XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,  
 PI Harthshorne TA, Suchorolski MT, Altus CM, Plets SJ, Elder LV;  
 PI Mooney EM, Delegeans AM, Panesar IS, Banville SC, Reddy TP;  
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;  
 PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;  
 PI Lagece RE, Spito PA, Stewart EA, Wingrove J, Vilec UA, Kirton BS;  
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;  
 PI Patury S, Shi X, Suarez CJ;  
 XX  
 DR MPI: 2004-329368/30.  
 DR N-PSDB; ACN42298.  
 XX  
 XX New diagnostic and therapeutic polynucleotides and polypeptides, useful  
 PT in diagnosing a condition, disease or disorder associated with human  
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
 XX in gene mapping.  
 XX  
 PS Claim 27; Page; 190pp; English.  
 XX  
 XX The invention relates to novel diagnostic and therapeutic polynucleotides  
 CC selected from one of the 2722 sequences defined in the specification. A  
 CC polynucleotide of the invention may have a use in gene therapy. The human  
 CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be  
 CC used to diagnose a particular condition, disease or disorder associated  
 CC with human molecules, e.g. cell proliferative disorders,  
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine  
 CC disorder, neurological disorders, gastrointestinal disorders, or  
 CC infections caused by virus, bacteria, fungi or parasite. The dithp  
 CC molecules may also be used in genetic mapping, in identifying individuals

CC from minute biological samples, in detecting single nucleotide  
CC polymorphisms, as molecular weight markers, and for somatic or germline  
CC gene therapy. The present sequence represents a d1tp protein of the  
CC invention. Note: The sequence data for this patent is not represented in  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)

XX Sequence 1722 AA;

Query Match 41.6%; Score 1674.5; DB 8; Length 1722;  
Best Local Similarity 46.4%; Pred. No. 3,9e-118;

Matches 356; Conservative 128; Mismatches 175; Indels 109; Gaps 16;

QY 4 GGNIKVVRVVRPNNAEIDRGACIVMEGNQITLPPGAERKARKSGKTMDGPKAFA 63  
DB 3 GASVKAARVRPNRSRMSRDSKCIIOGSGSTTTIVNPKPKET-----PKSFS 51  
QY 64 FDRSYWSPDKNAP--NYARQEDLPDLGVPLLDNAFKYNNCFAYGOTGSGKSYWVG 120  
DB 52 FDSYWS--HTSPEDINVASQKQVRYDIEMLQHAEGYVNCIFAYGOTGAGKSYWVG 109  
QY 121 YGK--EHGVIPIRCOMFRINELQDKNLCTVEVSYLEYINERVDLNPSTKGNLKY 178  
DB 110 KQKDDQGIIPOLCEDLFSRINDTTND--NMSYSVEVSYMEICERYRDLNPNKGNLRY 168  
QY 179 REHPTGTPYVEDLAKLVRSFOEINLMDGKNKARTVAATNNMETSSRSRAVFTLLTQK 238  
DB 169 REHPTGTPYVEDLAKLVRSFOEINLMDGKNKARTVAATNNMETSSRSRAVFTLLTQK 228  
QY 239 WHDEFTMDTEKVAKISLVLDLASERATSTGATGARKLKEGAEINRSLSLGRVYALADM 298  
DB 229 RHDATNITTEKYSKISLVLDLASERADSTGAKTRLEKAGINIKSLTIGKVIYSLAEM 288  
QY 299 ---SSGKQKQKQVPRRDSVLTWLKDSLCGNMTAMIAISPADINFEETLSLRYADS 355  
DB 289 XRPQNKKKKTDPIPYRDSVLTWLKRENLGNSRTIMVVALSPADINYDTLSLRYADR 348  
QY 356 AKRIKHAHVNEEDPNARMIRELKEBELAOLSKLOSQGGG-----GGAG----- 399  
DB 349 AKQIRCAVAVNEEDPNKMLRELKDEYTRLDLYAOGLDITTTNTVPGGPKVYSLDENN 408  
QY 400 --GSGGPEVESYPDPLEKQIVSIQOPDATVKKMS-----KAEIVE 439  
DB 409 NLRRGGTVNEAPDPLSTVTVNALVGM--SPSSSLALSRAVSLSLHRLIFAPGSEALIE 467  
QY 440 QLNQSEKLRDLNQTMEKLAKEBEIHKEREALEBELGISIER--GFVGPHSKEMPHLY 497  
DB 468 RLKETEKIITAEINLETWBEKLRTEAIRMERELALLAEMGVAMREDGGTLGVFSPKTPIHV 527  
QY 498 NLSDDLAECLVYNTKPGOTRYGANNQDTQAEIRLNGSLILKEHCTFEV-----VDNVV 552  
DB 528 NLNEDPLMSCLLYIKDITRGREGGERKQIVLSGFIKEKHCFRDSRGSSEAVV 587  
QY 553 TIVPNEKAAMVNVGVNIDKPTRLSRGYRIITLGFHIFRPNHPEAEAROEQSLNHSVT 612  
DB 588 TLEPGGADTVYVNGKVTESILRSGNRIIMGSHVFRFHPHQAQOERR-----638  
QY 613 NSOLGSPAERHRTLSKAGSDADGDSRSDPLPHFRGKDSDFVARRAASAILGLDOK 672  
DB 639 -----TPCAETPAEPVDVAFARLEILER--QGIDMK 667  
QY 673 ISHLTDELDALEFDVQKAAVARGLEVNEDESDSSFPVRDKYSN 720  
DB 668 --QEMORLOLEDOYRREEREATYILE--QORLDYSEKLEALOKQKDS 712

RESULT 8  
ABM83650 standard; protein; 1708 AA.

XX ABM83650;  
XX 18-NOV-2004 (first entry)

XX Human diagnostic and therapeutic protein SEQ ID NO:3899.

DE gene therapy; human diagnostic and therapeutic polynucleotide; d1tp.

XX Homo sapiens.

XX MO2004023973-A2.

XX 25-MAR-2004.

XX 12-SEP-2003; 2003MO-US028227.

XX 12-SEP-2002; 2002US-0410259P.

XX 12-SEP-2002; 2002US-0410260P.

XX (INCY-) INCYTE CORP.

XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,  
XX Harthorn TA, Suchorolski MT, Altus CM, Pits SJ, Elder LV,  
XX Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP,  
XX Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH,  
XX Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL,  
XX Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Katron ES,  
XX Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D,  
XX Patury S, Shi X, Suarez CJ,

XX WPI; 2004-329368/30.

XX N-PDB; ACN42302.

XX New diagnostic and therapeutic polynucleotides and polypeptides, useful  
XX PT in diagnosing a condition, disease or disorder associated with human  
XX PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
XX PT in gene mapping.

XX Claim 27; Page; 190p; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides  
XX CC selected from one of the 2722 sequences defined in the specification. A  
XX CC polynucleotide of the invention may have a use in gene therapy. The human  
XX CC diagnostic and therapeutic polynucleotides (d1tp) or polypeptides may be  
XX CC used to diagnose a particular condition, disease or disorder associated  
XX CC with human molecules, e.g. cell proliferative disorders,  
XX CC autoimmune/inflammatory disorder, developmental disorder, endocrine  
XX CC disorder, neurological disorders, gastrointestinal disorders, or  
XX CC infections caused by virus, bacteria, fungi or parasite. The d1tp  
XX CC molecules may also be used in genetic mapping, in identifying individuals  
XX CC from minute biological samples, in detecting single nucleotide  
XX CC polymorphisms, as molecular weight markers, and for somatic or germline  
XX CC gene therapy. The present sequence represents a d1tp protein of the  
XX CC invention. Note: The sequence data for this patent is not represented in  
XX CC the printed specification, but was obtained in electronic format directly  
XX CC from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)

XX Sequence 1708 AA;

Query Match 41.5%; Score 1673; DB 8; Length 1708;  
Best Local Similarity 46.9%; Pred. No. 4,9e-118;

Matches 353; Conservative 124; Mismatches 175; Indels 100; Gaps 14;

QY 4 GGNIKVVRVVRPNNAEIDRGACIVMEGNQITLPPGAERKARKSGKTMDGPKAFA 63  
DB 3 GASVKAARVRPNRSRMSRDSKCIIOGSGSTTTIVNPKPKET-----PKSFS 51  
QY 64 FDRSYWSPDKNAP--NYARQEDLPDLGVPLLDNAFKYNNCFAYGOTGSGKSYWVG 120  
DB 52 FDSYWS--HTSPEDINVASQKQVRYDIEMLQHAEGYVNCIFAYGOTGAGKSYWVG 109  
QY 121 YGK--EHGVIPIRCOMFRINELQDKNLCTVEVSYLEYINERVDLNPSTKGNLKY 178  
DB 110 KQKDDQGIIPOLCEDLFSRINDTTND--NMSYSVEVSYMEICERYRDLNPNKGNLRY 168  
QY 179 REHPTGTPYVEDLAKLVRSFOEINLMDGKNKARTVAATNNMETSSRSRAVFTLLTQK 238

Dd	169	REHPLGLPYVEDUSKLAIVTSYNDI	ODLMSGKAKARTVAATNNETSSSHAVFNITFOK	228	
Qy	239	WHEETKMDTEKAKAKISLVYDLAGESE	ATSTGATGARLKEGAENRSLSTLGRVIAALAD	298	
Dd	229	RHDAENITTEKYSKISLVYDLAGESE	ADSTGAKGRRLKEGANINNSLTTLCKVISA	288	
Qy	299	SGG----	KOKKQOLVPRYDSVLTWLLKOSL	CGNSMTAMIAAISPADINFEETLSTLRYA	355
Dd	289	DSQPNKKKKKKKTD	FIPIYRDSVLTWLLRRLNLCGNSRTAMV	VALSPADINDETTLSTLRYA	348
Qy	354	DSAKRIKNHVVNVEDNNA	MIRELKEELQLSKLSQSGGGGGGSGSG	GGVVESEYDPDT	413
Dd	349	DRAKQIRCNVNI	VEDNNKILRELKQVETRLDLV----	-AQQGIDITDTNTPVPG	400
Qy	414	PLEKQIVSIQOPDATYK	KKMS-----	KAEIVEQLANSEKLYRLDNLQTW	455
Dd	401	PXLTNLVGMSPESSLS	ALSSRAASVSLHERILFAPGSEEA	IELKXTKEIKINELNBTW	466
Qy	456	EBKLAATKEIHKEREAL	EBLGISLEK--GVQPYHSEKMPHLVNL	SDDPLLAELGYNI	513
Dd	461	EEKRLRTEALRMEREA	LLLEMGVAMREDGTLGVFSPKTPHL	VNLINDEPILMSECLLYYI	520
Qy	514	KPGQTVGNNO	NOTOAEIRLNGSKTLKECTEEN----	VDNVYIVNEKKAAMVNGVR	566
Dd	521	KDQITRAGREDGER	RODIVLSGHFIKEEHCVRSRSGSEAV	VYLFECBAQDYVNGKK	580
Qy	569	IDKPTRLSGYRIIL	GDPHIFRPNHPEEARERQCSLLRHS	VTNSQLGSPAPGRHRTL	628
Dd	581	VTEPSILRSNGR	LIMKSHVFRNHPQARQBER-----		615
Qy	629	SKAGSDADGDSRSD	SPLPHFRGKDSQWIFYARREASAIL	GLDQKISHLTDELALFDV	686
Dd	616	-----	-----TCAETPAEPVDMAPAQELLEK--	QGIDMK--QEMQRLQLEBDQY	658
Qy	689	QKARAVRGLVEDNE	DSQSSSPVARDKTKMSN	720	
Dd	659	RREREATYLL	E--QORLDYESKLEALQKOMS	689	

RESULT\_9

ABM83651

ID

ABM83651 standard; protein; 1699 AA.

XX

ABM83651;

XX

18-NOV-2004 (first entry)

DE

Human diagnostic and therapeutic protein SEQ ID NO:3900.

XX

gene therapy; human diagnostic and therapeutic polynucleotide; dntp.

XX

Homo sapiens.

OS

XX

MO2004023973-AA2.

PN

XX

25-MAR-2004.

PD

XX

12-SEP-2003; 2003MO-US028227.

PF

XX

12-SEP-2002; 2002US-0410259P.

PR

XX

12-SEP-2002; 2002US-0410260P.

XX

PA

(INCY-) INCYTE CORP.

XX

Schmidt JP, Wright RJ, Bruns CM, Marinovic MM, Shen F, Henthorn TA, Suchorolski MT, Altue CM, Plets SJ, Elder LV, Mooney EM, Deleagne AM, Pansar IS, Banville SC, Reddy TP, Stevens KA, Blanchard JL, Pansar SR, Wang X, Au AP, Gerstin EH, Paralta CH, Anderson SB, Rieux P, Shen EJ, Wu MC, Stuve LT, Lagace RE, Spiro PA, Stewart EA, Wingrove J, Viltz UA, Kitron ES, Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson UL, Gletzen D, Patury S, Shi X, Suarez CJ;

XX	WPI: 2004-329368/30.
DR	N-PSDB; ACN42303.
XX	
XX	New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT	in diagnosing a condition, disease or disorder associated with human
PT	molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT	in gene mapping.
XX	
PS	Claim 27; Page; 190pp; English.
XX	
CC	The invention relates to novel diagnostic and therapeutic polynucleotides
CC	selected from one of the 2722 sequences defined in the specification. A
CC	polynucleotide of the invention may have a use in gene therapy. The human
CC	diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be
CC	used to diagnose a particular condition, disease or disorder associated
CC	with human molecules, e.g. cell proliferative disorders,
CC	autoimmune/inflammatory disorder, developmental disorder, endocrine
CC	disorder, neurological disorders, gastrointestinal disorders, or
CC	infections caused by virus, bacteria, fungi or parasite. The dthp
CC	molecules may also be used in genetic mapping, in identifying individuals
CC	from minute biological samples, in detecting single nucleotide
CC	polymorphisms, as molecular weight markers, and for somatic or germ-line
CC	gene therapy. The present sequence represents a dthp protein of the
CC	invention. Note: The sequence data for this patent is not represented in
CC	the printed specification, but was obtained in electronic format directly
CC	from WIPO at <a href="http://www.wipo.int/pct/en/sequences/listing.htm">www.wipo.int/pct/en/sequences/listing.htm</a>
XX	
SO	Sequence 1699 AA:
Query Match	41.4%; Score 1669.5; DB 8; Length 1699;
Best Local Similarity	46.8%; Pred. No. 8.9e-118;
Matches 352;	Conservative 125; Mismatches 166; Indels 109; Gaps 15
OY	4 GGNKVVVVRVPPNAREIDRGAKCIVRWEGNOTILTPPGAEBKARKSGKTMIDGPKA 63
DB	3 GASYKVAARVAPFNSREMSRDKSCITQWGSITTIIVNPKPKET-----PKFS 51
OY	64 FDRSYWSPDKAP---NYARQEDLFODLGVLLDPAFGYNNICFAYGOTGSGKSVMWG 120
DB	52 FDSYVWS--HNSPEDINVASQKYVRDGEMLQAFGYNVCIFAYGOTGAGKSYTMWG 109
OY	121 YGK--EHGVIPRICQDMFRINELQDKNLTCTVEVSYLYEINERKVDLNPSTGNLKV 178
DB	110 KQEKDQGGIIPQLCEDLFPSRINDTND--NMSYSVEVSYMEIYCEVRDLNPKNGNLRV 168
OY	179 REHSTGPGYVDLKLTVRSFOELENLDEGNKARTVAATMMNERSSHAVFTLLQK 238
DB	169 REHPLGLGYVDLSKLATVSTINDIQLDMSGNKARTVAATMMNERSSSHAVFNIIIPQK 228
OY	239 WHDEETKQDTEKVKAKISLVLDAGEBRATSTGATGARLKEGAEINRSLSLTLGRVIALADM 298
DB	229 RHDAETNITTEKVKISLVLDAGEBRADSTAGKGRLEKGANINKSLTLTKVISALAEW 286
OY	299 SSG-----KQKNQOLVPYRDSVLTWLLKDSIGGNSMTAMIAISPADINFEETLSLRYA 353
DB	289 DSGPNKKKKKKKTDFIPIYRDSVLTWLLRENLGGNSRTAMVAALSPADINVEETLSLRYA 348
OY	354 DSARKIRKHAIVNNDPNAKMTRELKELAOURLSKLQSSGGGGGAGGSGGCPVEESYPPDT 413
DB	349 DRAQOIRNAIYNIDPNKKLIRELKDEVTRLRLDLYAAGIG-----DIT 392
OY	414 PLEKQIVSIQOPDRTVKKMS-----KAEIVQOLNSEKLYRDLNQTW 455
DB	393 DMTAALVGM--SPSSLSLASSRAASVSSLHRLIPAPSEBAERLKEKTEKIIALNELRW 451
OY	456 EEKLAKTEELIKEREAALDELGISIEK--GFVGPYHSKEMPHLVNLSDDPLLAELGLVNI 513
DB	452 EEKURLRTEALIMEREDALLAEKGVAMREDGGTLGVFSPKKTDLVLVNLNEDPLMSSECLAYI 511
OY	514 KPGQTRGVANNQDTQAEIRLNGSKILKEHCTFEN-----VNVVTVIVNEKAAVNVNVR 568
DB	512 KDGTTRVREGREGBERODIVLGGHTEIKESHCVFRSDSRGSGSAVVTLPECEGADIVVNGK 571

Qy	569	IDKPRLSGVYIIIGDFFIPEFNHPEEARARQSGSLRHSVTSQSGSPARGHRTL	628
Db	572	VTEPSILNSGNRIINGKSHVFRFNHPEQKQRRER-----	606
Qy	629	SKAGSDADGDSRSDPLPHFRGKSDSWFYARREASAILGLDQKISHLTDELDLFDV	688
Db	607	-----TPCAETPAEPVDMAFAGRELELK-QGIDMK--QMEGRQLGLEDDY	649
Qy	689	QKARAVRGLVEDNEDSDSGSPFYPRDKTMSN	720
Db	650	RREREATYLL-QQRLDYESTKLEALQKQWDS	680
RESULT 10			
AAB36227			
ID	AAB36227	standard; protein; 1816 AA.	
XX	AAAB36227;		
XX	AC		
XX	DT	19-FEB-2001 (first entry)	
XX	DE	Human kinesin-like protein HKLP SEQ ID NO: 4.	
XX	KW	Human; kinesin-like protein; HKLP; KIF1; cell division; cancer;	
XX	KW	intracellular transport; neurological disorder; infertility;	
XX	KW	biological marker; spontaneous abortion; neonatal chromosome disorder;	
XX	KW	aneuploidy.	
OS	Homo sapiens.		
FN	MO200063375-AI.		
XX	PD	26-OCT-2000.	
XX	PF	20-APR-2000; 2000WO-IB000562.	
XX	PR	20-APR-1999; 99US-0130217P.	
PA	(GEST ) GENSET.		
XX	FI	Bougueleret L, Dufaire-Gare I, Grel P;	
XX	DR	WPI; 2000-665242/64.	
XX	DR	N-PSDB; AAC66550.	
PT	PT	An isolated or purified human kinesin-like protein (HKLP) encoding	
PT	PT	polynucleotide used to detect HKLP polynucleotides in a sample comprises	
XX	XX	a contiguous span of at least 12 nucleotides.	
PS	XX	Claim 46; Page 189-192; 1999p; English.	
CC	XX	The present invention describes the coding and protein sequences of the	
CC	XX	human kinesin-like protein HKLP. It is thought that the protein could be	
CC	XX	involved in neurological disorders, infertility, spontaneous abortion,	
CC	XX	neonatal chromosome disorders, aneuploidy and cancers. This is due to its	
CC	XX	function in the movement of microtubules. The protein shows homology to	
CC	XX	the murine KIF1A and KIF1B proteins. The sequences disclosed in the	
CC	XX	invention can be used in the isolation of similar human proteins and in	
CC	XX	vector production. In addition, the diallelic markers shown can be used	
CC	XX	in disease diagnosis and population studies	
SO	Sequence	1816 AA;	
Qy	Query Match	41.4%; Score 1668.5; DB 3; Length 1816;	
Db	Beet Local Similarity	45.0%; Pred. No. 1.2e-117;	
	Matches	356; Conservative 126; Mismatches 172; Indels 137; Gaps 16;	
Qy	4	GNINIVVAVRPPFNAREIDRGAKCTIVRMENQOTILTPPGAEBEKARKSGKTIIMDGPKAPA	63
Db	3	GASVAVNARVAVRPPFNARETSKESKCTIIMQGNSTSIINKNPRE-----APKSF	51
Qy	64	FDRSYWTF-DKKAPVYARQEDLFQDLGVPLLDNAFKYNNCTIPAYGQTGSGKSYSMGYG	122

Db	52	FDYSTWSTHSPEPDPCFPASGNRYVNDIGKXMLHAFEGVVCIFAYQGTAGASYTMGQ	111
Qy	123	KEH--GVIPLRCQDMFRRINELQKKNLCTVEVSYLIEYNERVDDLNPSTGNKVRE	180
Db	112	BESQAGIILPOLCEBELPEKIND-NCNEMBSYSEVSYMEYLCEVRDLDPKKNGLRVRE	170
Qy	181	HPSTPPEYEDLAKLVYRSPQEIENIMDSGNKARVTAATMMNETSSSHAVFTLTQKH	240
Db	171	HPLLPPYVEDLSKLAVTSTYTDIADLMDADNKKARTVAATMMNETSSSHAVFTVFTQKH	230
Qy	241	DEETGMDEKAKISLVLDAGSERATSTGATGARLKEGAEINRSLSTIGRVIAALDM--	298
Db	231	DNEITLSTEEKSKISLVLDAGSERADSTGAKTRLEGNANINSLTTLGLGVLSALLEVDN	290
Qy	239	---SSGKKQKQVLVYRDSVLTWMLKDSLIGNSMTAMIAISPADINFEETLSTLYVAD	355
Db	291	CTSKSKKKKKKTDFIYRDSVLTWMLRENNGSRMTAVALSADINYEETLSTLYADR	356
Qy	356	AKRIKNAHVNEDPNARMIRELKEELADQLRSTLQSSGGG-----GGAG-----	399
Db	351	AKQIKNAVINEDPNAKLVRELKEEVTRLKDLRAQGLGDIIDIDPLIDYSGSGSKYLK	410
Qy	400	-----GGGPRPEEYPPDTPLEKQ-----LYSIQPPDAIVKK	431
Db	411	DFQNNKHRYLLASENQRGHFSTAGMSLTSS-PSSCSLSSQVGLTSVTSIQ--ERIMST	467
Qy	432	MSKAEIVQLNOSKLYRDLNQTMEELKATEIEHKEREALAEIGISTEK--GVFGPNY	489
Db	468	PGGEAIRLERLKESEKTIAMELNETWEEKLRKTAIMERALLAEKVAALREDDGTLGVRS	527
Qy	490	SKEMPHLVNLSDDPLLAELCVYNIKPGQTRGVANVDQTQAEIRLNGSKILKEHCTPENV-	548
Db	528	PKTTPHLVNLNEDPLMSECLLYIYIKDGIITRVQGADEARQDLYLSGAHIKEBHCPRESR	587
Qy	549	----DNVTIYIPNEQAIVMVGVRIDKPRRLASGTRILGDIHIFPFNPEEARARQEQ	604
Db	588	SNSGVIYTLTEPCERSETTYVNGKRVSPQVLNSGRITIMGNKHVFEPNPEQARAREK-	646
Qy	605	SLLRHSVNSQLSGSPAPGRHDTTSLKAGSDADGSDSDSPFLPHFRKQDMFYAREEAS	664
Db	647	-----TPSAETPSEPDWTFPAQELLE	668
Qy	665	AILGLDQK-----ISHLTDELDALFDD-----VQKARAVRRLVED	701
Db	669	K-QGIDMKQEMEKRLQEMELIYKKEKEEADLLLEQGRDYESKQLQKOVERSLAET	727
Qy	702	NEDSDQSQSPF	712
Db	728	TEEEEEEVEVP	738
RESULT 11			
ADJ95088			
ID	ADJ95088	standard; protein; 1805 AA.	
AC	ADJ95088;		
DT	06-MAY-2004	(first entry)	
DE	Novel NOVX protein sequence #158.		
XX	antidiabetic; anorectic; cardiac; hypotensive; antiarteriosclerotic;		
KM	anorectic; vinuclide; antibacterial; fungicide; protozoacide; nootropic;		
KM	neuroprotective; antiparkinsonian; anticonvulsant; osteopathic;		
KM	antiatherogenic; antiinflammatory; dermatological; antistomatia;		
KM	antiileptic; gene therapy; metabolic disorder; diabetes; obesity;		
KM	infectious disease; anorexia; cancer; cardiovascular disease;		
KM	hyperextension; atherosclerosis; neurodegenerative disorder;		
KM	Alzheimer's disease; Parkinson's disease; epilepsy; immune disorder;		
KM	osteoarthritis; hematopoietic disorder; inflammatory skin disorder;		
KM	asthma; dyslipidemia; neurogenesis; cell differentiation;		
KM	cell proliferation; hematopoiesis; wound healing; angiogenesis;		



Db 468 IERLKESEKIIAEINETWESEKLRKTEAIRMERALLAEMGVAIREDDGTLGVFSPKPTPH 527  
Qy 496 LVNLSDDPLAECGLVYNIKPQOTRVGNVNDTOAEIPLNSKILKEHCTENV-----DN 550  
Db 528 LVNLSNEDPLAECGLVYNIKPQOTRVGNVNDTOAEIPLNSKILKEHCTENV-----DN 550  
Qy 551 VVTIVPEKAAMVWNGVRIDKPTLRSGYRIILGDFHIFRNHPEERAROEQSLRH 610  
Db 588 IVTLPEPERSEYVNGRVSGPQVLRSGNRIIMKGNHVFERNHPEQARERK----- 640  
Qy 611 VTNLSQSGPAPGRHRTLSKAGSDADGSDSPPLPHFRKSDWFIYARREASAILGLD 670  
Db 641 -----TPSAETPSEPVDTWTFARQELLEK-QGID 667  
Qy 671 QK-----ISHLTDELALFDD-----VQKARAVRGLVEDNEDSDS 707  
Db 668 MKQEMERKLOEMELLYKKEKEADLLLEQRLDYESKLQALQKQVETRSILAETTEEBE 727  
Qy 708 QSSFP 712  
Db 728 EEEVP 732

RESULT 12  
AAE35317  
ID AAE35317 standard; protein; 1770 AA.  
XX  
AC AAE35317;  
XX  
DT 17-JUN-2003 (first entry)  
XX  
DE Mouse KIF1Bbeta protein.  
XX  
KW KIF1B protein; gene therapy; molecular motor protein; kinesin; mouse;  
KW KIF1Bbeta gene-associated disease; Charcot-Marie-Tooth disease type 2A;  
KW muscular; transgenic.  
XX  
OS Mus musculus.  
XX  
PN MO200297079-A2.  
XX  
PD 05-DEC-2002.  
XX  
PF 29-MAY-2002; 2002MO-JP005226.  
XX  
PR 29-MAY-2001; 2001US-0293513P.  
XX  
PA (UYTY ) UNIV TOKYO.  
XX  
PI Hirokawa N, Hayaehi Y;  
XX  
DR WPI, 2003-167270/16.  
XX  
DR N-PSDB; AAD53964.  
XX  
PT New KIF1B polypeptide having motor activity that transports synaptic  
PT vesicle precursor, is useful for developing therapeutic or preventive  
PT agent for kif1b gene-associated diseases e.g. Charcot-Marie-Tooth  
PT disease type 2A.  
XX  
PS Claim 1; Page 72-78; 44p; English.  
XX  
XX The invention relates to KIF1B protein which belongs to kinesin  
CC superfamily of molecular motor proteins (KIFs). KIF1B is useful for  
CC screening for a compound binding to it. Composition comprising the  
CC selected compound is useful for treating, alleviating, or preventing a  
CC KIF1B gene-associated disease, in particular Charcot-Marie-Tooth  
CC disease type 2A. Transgenic non-human vertebrate, are useful for  
CC screening for a candidate compound for treating, alleviating, or  
CC preventing a KIF1B gene-associated disease. KIF1B DNA is useful for  
CC gene therapy and for recombinant production of polypeptides. KIF1B  
CC antibody is useful for affinity purification of KIF1B and for detecting  
CC expression of KIF1B gene at the protein level. The present sequence  
CC is mouse KIF1Bbeta protein

XX  
SQ Sequence 1770 AA;  
Query Match 41.4%; Score 1666.5; DB 6; Length 1770;  
Best Local Similarity 47.3%; Pred. No. 1,6e-117;  
Matches 353; Conservative 125; Mismatches 174; Indels 95; Gaps 15;  
Qy 4 GGNIKYVVRPRPNARERIDGACIYRMENQIILTRPPAEKARSKGTINDGPAFA 63  
Db 3 GASVKAARVRPPNSRSEKSCIIQMOGNSSTSIINPKPKB-----APKSF 51  
Qy 64 FDRSYMSF-DKNAFNPAREDELFQDLGVPLDPAFGYNNICPAYCOTSGSKSYMWG 122  
Db 52 FDYSYMSHSPEDPCASQNRVYNDIGKMLHAFEGYVNCIFAYCOTSGSKSYTWGK 111  
Qy 123 KEH-GVIRICODMFRRIEOLKXNLCTYVSYLEYNEVRDLNPTGNTKVR 180  
Db 112 EESQAGIIPOLCELEPEKIND-NCNEMSYSVSVSYMEICYERVRDILNPKGNLRVRE 170  
Qy 181 HPSTGPIVEDLAKLVYRSFOEINLMDGKATVAATNNETSSRSNAVFTLTQKH 240  
Db 171 HPLGPIVEDLSKLAVTSTYDIADLMDAGKATVAATNNETSSRSNAVFTLTQKH 230  
Qy 241 DEETKMDTEKVAKISLVDLAGESEATSGATGARLKEGAEINRSLSLGRVIAALDMS 300  
Db 231 DEPTNLSTKSVKISLVDLAGESEATSGATGARLKEGAEINRSLSLGRVIAALDMS 290  
Qy 301 GKQKQOLVPRYDVLTWLLKDSLGNSMTAMIAISPADINEFTLSTLYVADSARIK 360  
Db 291 -KKKTDPIPRYDVLTWLLRENLGNSRTAMVAPALSPADINDEFTLSTLYVADRAKQ 349  
Qy 361 NHAVNVEDPVARIRIRLKEELADLRKLSGSGGSGGAGSGGPVESEYPTPLEKQ-- 418  
Db 350 CNAVINEDPVARIRIRLKEELADLRKLSGSGGSGGAGSGGPVESEYPTPLEKQ-- 407  
Qy 419 ---IVSIQPDATVKKMSAEIYEQUNOSEKLYRDINOTWEKTLAKTEIRHKEEAL 475  
Db 408 LTVSTSIQ-ERIMSTPGGEAEIRLKESEKIIAEINETWEKTLAKTEIRHKEEAL 465  
Qy 476 LGISIEK-GVQGYHSMKEMPHLVNLSDDPLAECGLVYNIKPQOTRVGNVNDTOAEIRL 533  
Db 466 MGVAIREDDGTLGVFSPKPTPHLVNLSDDPLAECGLVYNIKPQOTRVGNVNDTOAEIRL 525  
Qy 534 NSGKILKEHCTENV-----DNVVTIVPEKAAMVWNGVRIDKPTLRSGYRIILGDFH 568  
Db 526 SGAKIIEHCLFRSERSNTGEVIVTLPEPERSEYVNGRVAPVQLRSGNRIIMKGNH 585  
Qy 589 FRNHPERAREROEQSLRHSTVNSQLGSPAPGRHRTLSKAGSDADGSDSPPLPH 648  
Db 586 FRNHPERARERK-----TPSAET 606  
Qy 649 RGDSDWFIYARREASAILGLDQK-----ISHLTDELALFDDVQK 691  
Db 607 PSEPVDTWTFARQELLEK-QGIDMKQEMERKLOEMELLYKKEKEADLLLEQRLDYESTL 665  
Qy 692 RAYRGL-----VEENEDSDQSFP 712  
Db 666 QALQKQVETRSILAETTEEBEVEVP 692

RESULT 13  
ABB07867  
ID ABB07867 standard; protein; 1823 AA.  
XX  
AC ABB07867;  
XX  
DT 03-JUL-2002 (first entry)  
XX  
DE Human kinesin-associated protein having motor domain.  
XX  
KW Human; kinesin-associated protein; motor domain; cytoskeletal; KIF1B-beta;  
KW neuroblastoma.  
XX





CC encoded polypeptides (AAM3642-AAM42213) with nootropic,  
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC localised neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilisation of the activities such as: Immune system suppression,  
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukaemias and  
 CC C.N.S disorders. Note: The sequence data for this patent did not form  
 CC part of the printed specification

XX  
 XX  
 SQ Sequence 893 AA;

Query Match 41.2%; Score 1660.5; DB 4; Length 893;  
 Best Local Similarity 46.5%; Pred. No. 1.6e-117;  
 Matches 350; Conservative 126; Mismatches 167; Indels 109; Gaps 15;

QY 4 GGNIKYVVRPFPNAREIDRGAKCIVRMEGNOTILTPPBAEKARKSGKTINDGPAPA 63  
 DB 3 GASVKAVAVRFPNRSRMSRDSKCIIOGSGSTTTIVNPKPKET-----PKSFS 51  
 QY 64 FDRSYWSPDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGOTSGKSYSWMG 120  
 DB 52 FDSYSVA--HTSPEDINVASQKQVYRDIGBEMIOHAFEGNVCIFAYGOGAKSITMKG 109  
 QY 121 YGK-EHGVIPRICQMFRRINELQDKMLTCTVEVSYLEIYNERVADLLNPSTKGLKY 178  
 DB 110 KQEKDQGGIIPOLCEBDFSRINDTND-NMSYSVEVSMEIYCEVRADLLNPKKGLRY 168  
 QY 179 REHPSRGPVYEDLAKLVNRSFOEINLMDGKARKYAAANNMETSRSRAVTLITLTK 238  
 DB 169 REHPLLPVYEDSKIAVTSYNDIOQDMOSGNKARKYAAANNMETSRSRAVFNIIFTOK 228  
 QY 239 WHDEETKMDTEAKISLVLDLASERATSGATGARLKEGAEINRSISTGRVIALADM 298  
 DB 229 RHAENITTEKSKISLVLDLASERADSTGAKTRKEANINKSLITLTKVISAIAEM 288  
 QY 299 SSG-----KQKNQVLVPRDSVLTWLLKDSLGNSMTAMIAISPADINEETLSTLRYA 353  
 DB 289 DSGPNKKKKKKTKDFIPYRDSVLTWLLREVLGNSRTAMVAALSPADINDETSLTRYA 348  
 QY 354 DSAKRIKNAVNVEDNARMIRLEKEELAQTRKLGSSGGGGGAGSGGAPVEESTPPT 413  
 DB 349 DRAKQIRCAVNVEDNPNKILRELKQBYRLDLVLAQGLG-----DIT 392  
 QY 414 PLEKQIVSIQOPATVYKNS-----KAEIYEOJNOSEKLYRDLNOM 455  
 DB 393 DMYNALVGM-SPSSSIALSSRAASVSLHERLLPAPGSEAEIRLEKTEKTIABINETW 451  
 QY 456 EKKLAETIEIHKERALEELGISIEK--GFVGRYHSEKMPHLVNLSDPLLAECVYNI 513  
 DB 452 EKKLRTEAIRMERREALLMEVGAEMKEDGTLGVFSPKTPHLVNLNEDPLMECLLYI 511  
 QY 514 KPGQTVANNNOTQAEIRLNGSKILKEHTFEN-----VDNVYTVNPKAAVMMNGVR 568  
 DB 512 KQGITVGRDEGRRDQIVLSGHFIRKEHCVFSDSGSEAVVLEPFCGATYVNGKK 571  
 QY 569 IDKPTRLSGSYRIILGDFHIFRNHPPEBARERQOGLLRHSTNQLSGPAGRHDRTL 628  
 DB 572 VTRPSILRSGNRILMGKSHVFRTHPEQARKER----- 606  
 QY 629 SKAGSDADSDSRSDPLPHFRGSDMFWARREASAILGLDQKISLTDDELALFDDV 688  
 DB 607 -----TCAETPAEPVDMWAFQRELLEK--QGIDMK--QEMEQRLQELDDY 649  
 QY 689 QKARAVRGLVEDNEDSDSSSPVADKYMSN 720  
 DB 650 RRREAEATYLE-QORLDYESKLEALQKOWDS 680

# RESULT 15

ABM83652  
 ID ABM83652 standard; protein; 1697 AA.

XX  
 AC ABM83652;

DT 18-NOV-2004 (first entry)

DE Human diagnostic and therapeutic pprotein SEQ ID NO:3901.

XX gene therapy; human diagnostic and therapeutic polynucleotide; dlthp.

OS Homo sapiens.

PN WO2004023973-A2.

PD 25-MAR-2004.

PF 12-SEP-2003; 2003MO-US028227.

PR 12-SEP-2002; 2002US-0410259P.

PR 12-SEP-2002; 2002US-0410260P.

PA (INCY-) INCYTE CORP.

PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,

PI Hartshorne TA, Suchorolski MT, Altus CM, Plets SJ, Elder LV,

PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP,

PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH,

PI Percalta RE, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;

PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Katon ES;

PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;

PI Patency S, Shi X, Suarez CO;

XX MPI; 2004-329368/30.

DR N-PSDB; ACN42304.

PT New diagnostic and therapeutic polynucleotides and polypeptides, useful

PT in diagnosing a condition, disease or disorder associated with human

PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or

PT in gene mapping.

PS Claim 27; Page; 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides

CC selected from one of the 2722 sequences defined in the specification. A

CC polynucleotide of the invention may have a use in gene therapy. The human

CC diagnostic and therapeutic polynucleotides (dlthp) or polypeptides may be

CC used to diagnose a particular condition, disease or disorder associated

CC with human molecules, e.g. cell proliferative disorders, endocrine

CC autoimmune/inflammatory disorder, developmental disorder, endocrine

CC disorder, neurological disorders, gastrointestinal disorders, or

CC infections caused by virus, bacteria, fungi or parasites. The dlthp

CC molecules may also be used in genetic mapping, in identifying individuals

CC from minute biological samples; in detecting single nucleotide

CC polymorphisms, as molecular weight markers, and for somatic or germline

CC gene therapy. The present sequence represents a dlthp protein of the

CC invention. Note: The sequence data for this patent is not represented in

CC the printed specification, but was obtained in electronic format directly

CC from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)

XX  
 SQ Sequence 1697 AA;

Query Match 41.2%; Score 1659.5; DB 8; Length 1697;  
 Best Local Similarity 46.7%; Pred. No. 5.2e-117;  
 Matches 350; Conservative 126; Mismatches 167; Indels 107; Gaps 15;

QY 4 GGNIKYVVRPFPNAREIDRGAKCIVRMEGNOTILTPPBAEKARKSGKTINDGPAPA 63  
 DB 3 GASVKAVAVRFPNRSRMSRDSKCIIOGSGSTTTIVNPKPKET-----PKSFS 51  
 QY 64 FDRSYWSPDKNAP---NYARQEDLFQDLGVPLLDNAFKGYNNCIFAYGOTSGKSYSWMG 120

```
Db 52 FDYSYMS--HTSPEDINVASQKVVRDISEBMLQHAFBEGYNVICIFAYGQTGAGKSYTMWG 109
Qy 121 YGK--EHGVIPRI CODMFRRINELOKKULCTVEVSYLEIYNERVRDLLNPSTKGNLKV 178
Db 110 KQEKDQOGIIPOLCEDLFGRINDTND-NMSYSVEVSYMEIYCERVRLDILNPKNGNLKV 168
Qy 179 RHPSTGPRVEDLAVLVNSFOEIENTLMDEGNKARTVAATNNNETSSRSHAVFTLLTLTK 238
Db 169 RHPPLGPRVEDLSKLAVTSYNDIOQLMBSGNKARTVAATNNNETSSRSHAVFNILFTOK 228
Qy 239 WHDEETKMDTEKYAKISLVDLAGESEATSGATGALKEGAEINRSLSLIGRYIALADM 298
Db 229 RHDATNITTEKYSKISLVDLAGESEADTGAKGTRLKEGANINKSLTLGKVISALAE 288
Qy 299 ---SSGKQKKNQLVPRYDSVLTWLNKDSLGSNSMTAIAISPADINFEETLSTERYADS 355
Db 289 XPPQNKKKKTDPIPRYDSVLTWLNRENLGNSRTAMVAAISPADINDETSLTRYADR 348
Qy 356 AKRIKNAHVNNEDPNARMTRELKEELAKLSKLGSSGGGGGAGSGSPVEESYPPDPL 415
Db 349 AKQIRCNNAVINEDPNKLIRELKDEVTRLRLDLVYAGLG-----DITDM 392
Qy 416 EKQIVSIQOPDATVKKMS-----KAEIVQLNQSEKLYRDLNQTWEE 457
Db 393 TNALVGM-SPSSSLALSRRASVSLSHERILFAPGSEAEIERLKETEKIAMELNETWEE 451
Qy 458 KLAETEEIHKERBALEELGISIEK--GFVGPYHSKEMPHLVNLSDDPLLAECLYYNIKP 515
Db 452 KLRTETAIHMEREBALAEWGVAMREBDGTLGVFSPKTPHLVNLNEDPLMSECLLYIKD 511
Qy 516 GQTRVGNVNOPTQAEIRLNGSKILKEHCPEFEN----VNVVTIVPNEKAAVWNGVRID 570
Db 512 GITRVGREDEGRQDVLGHPFKEHCVPFRSDRGSEAVVTLPECEGADTYVNGKKVY 571
Qy 571 KPTRLSGRIILGDPHIFRFNHPBEARAEBOESILRHSVTNSQLGSPAPGRHRTLSK 630
Db 572 EPSILRSSGNRIIMGKSHVFRFNHPBQARQERER----- 604
Qy 631 AGSDADGDSRSDPLPHFRGKSDWPFYARREASAILGLDQKISHLTDELALFDDVOK 690
Db 605 -----TPCAETPAEPVDMAFAQRELEK--QGIDMK--QEMEORLQLEBDQYRR 649
Qy 691 ARAVRGLVEDNEDSDOSSFPVRDKYMN 720
Db 650 ERBEATYLLLE-QORLDYESKLEALQKQWDS 678
```

Search completed: September 1, 2006, 14:27:10  
Job time : 194.583 secs

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: September 1, 2006, 14:22:42 ; Search time 263.166 Seconds  
(without alignments)  
2755.725 Million cell updates/sec

Title: US-09-235-416-1  
Perfect score: 4030  
Sequence: 1 MSGGNIKVVVRVPRNARE.....ELRQQAQMEALKTAKQER 784

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues  
Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: UniProt\_7.2.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3966	98.4	786	2 Q6IU06_THELA	Q6IU06 thermomyces
2	3216	79.8	1632	2 Q4X048_ASPRU	Q4X048 aspergillus
3	3168	78.6	1630	2 Q5AVY3_EMEXI	Q5AVY3 aspergillus
4	2842	70.5	1962	2 Q7S784_NEUCR	Q7S784 neurospora
5	2814.5	69.8	1087	2 Q86292_GIBMO	Q86292 gibberella
6	2773	68.8	1814	2 Q4HXW9_GIBZE	Q4HXW9 gibberella
7	2761.5	68.5	1793	2 Q862A3_COCHB	Q862A3 cochliobolus
8	2721	67.5	1666	2 Q2UE08_ASPOR	Q2UE08 aspergillus
9	2634	65.4	1519	2 Q4P0W2_USTVA	Q4P0W2 ustilago ma
10	1957.5	48.6	1676	2 Q8TG36_USTVA	Q8TG36 ustilago ma
11	1932.5	48.0	1556	2 Q55246_CRYNE	Q55246 cryptococcus
12	1895	47.0	1556	2 Q5KNG1_CRYNE	Q5KNG1 cryptococcus
13	1691	42.0	1153	2 Q4VXC3_HUMAN	Q4VXC3 homo sapien
14	1683.5	41.8	1797	2 Q4R9M8_HUMAN	Q4R9M8 homo sapien
15	1680.5	41.7	1770	2 Q4VXC5_HUMAN	Q4VXC5 homo sapien
16	1677	41.6	1161	2 Q8JIX1_BRARE	Q8JIX1 brachydanio
17	1676.5	41.6	1809	2 Q4R9M9_HUMAN	Q4R9M9 homo sapien
18	1673.5	41.5	1673	2 Q4R9M9_HUMAN	Q4R9M9 homo sapien
19	1673.5	41.5	1673	2 Q4R9M9_HUMAN	Q4R9M9 homo sapien
20	1672	41.5	1673	2 Q4R9M9_HUMAN	Q4R9M9 homo sapien
21	1672	41.5	1673	2 Q4R9M9_HUMAN	Q4R9M9 homo sapien
22	1670	41.4	1679	2 Q7PHR1_MOUSE	Q7PHR1 mus musculu
23	1669.5	41.4	1690	2 Q53I78_HUMAN	Q53I78 homo sapien
24	1669.5	41.4	1690	2 Q53I78_HUMAN	Q53I78 homo sapien
25	1669.5	41.4	1816	2 Q2NKA6_HUMAN	Q2NKA6 homo sapien
26	1669	41.4	937	2 Q5XK63_MOUSE	Q5XK63 mus musculu
27	1669	41.4	1100	2 KIFP1_MOUSE	KIFP1 mus musculu
28	1668.5	41.4	1689	2 Q6PSH4_MOUSE	Q6PSH4 mus musculu
29	1668.5	41.4	1689	2 Q6PSH4_MOUSE	Q6PSH4 mus musculu
30	1668.5	41.4	1816	2 Q4VXC6_HUMAN	Q4VXC6 homo sapien
31	1668.5	41.4	1823	2 Q4VXC4_HUMAN	Q4VXC4 homo sapien

32	1667.5	41.4	1816	1 KIF1A_RAT	O88658 rattus norv
33	1667	41.4	1103	1 KIF1C_HUMAN	O43896 homo sapien
34	1667	41.4	1120	2 Q6A011_MOUSE	Q6A011 mus musculu
35	1665	41.3	1103	2 Q5U618_HUMAN	Q5U618 homo sapien
36	1663.5	41.3	1690	1 KIF1A_HUMAN	Q12756 homo sapien
37	1663.5	41.3	1695	1 KIF1A_MOUSE	P33173 mus musculu
38	1660.5	41.2	1816	1 KIF1B_MOUSE	O60575 mus musculu
39	1659	41.2	1100	2 Q8V189_MOUSE	Q8V189 mus musculu
40	1657.5	41.1	628	2 Q3UY61_MOUSE	Q3UY61 mus musculu
41	1630.5	40.5	1671	2 Q9NBL1_DROME	Q9NBL1 drosophila
42	1629	40.4	1670	2 Q8MLF6_DROME	Q8MLF6 drosophila
43	1617	40.1	1097	1 KIF1C_RAT	Q35787 rattus norv
44	1611	40.0	1576	2 Q6IGJ3_CAEBR	Q6IGJ3 caenorhabdi
45	1590.5	39.5	1584	1 UN104_CAEBL	P23678 caenorhabdi

## ALIGNMENTS

## RESULT 1

Q6IU06\_THELA PRELIMINARY; PRT; 786 AA.  
ID Q6IU06;  
AC Q6IU06;  
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2004, sequence version 1.  
DI 07-FEB-2006, entry version 10.  
DE UN104/KIF1A-like protein (Fragment).  
OS Thermomyces lanuginosus (Humicola lanuginosa).  
OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Thermomyces.  
OX NCBI\_TaxID=5541;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Rivera S.B., Koch S.J., Bauer J.M., Edwards J.M., Bachand G.D.;  
RL Submitted (May-2004) to the EMBL/GenBank/DBJ databases.  
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CC  
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DR EMBL: AY623608; AAT39887.1; -; mRNA.  
DR GO: GO:0003874; C:mitochondrion; IEA.  
DR GO: GO:0005875; C:mitochondrion associated complex; IEA.  
DR GO: GO:0005524; F:ATP binding; IEA.  
DR GO: GO:0003777; F:mitochondrion motor activity; IEA.  
DR GO: GO:0000166; F:nucleotide binding; IEA.  
DR GO: GO:0007018; F:mitochondrion-based movement; IEA.  
DR InterPro: IPR001253; FHA.  
DR InterPro: IPR001752; kinesin\_motor.  
DR Pfam: PF00498; FHA; 1.  
DR Pfam: PF00225; Kinesin; 1.  
DR PRINTS: PR00380; KINESINHEAVY.  
DR SMART: SM00129; KISC; 1.  
DR PROSITE: PS00411; KINESIN MOTOR DOMAIN1; 1.  
DR PROSITE: PS0067; KINESIN MOTOR DOMAIN2; 1.  
KW ATP-binding; Mitochondrion; Motor protein; Nucleotide-binding.  
FT NON TER 786  
SQ SEQUENCE 786 AA; 87201 MW; A008023FBAA70312 CRC64;

Query Match 98.4%; Score 3966; DB 2; Length 786;

Best Local Similarity 98.9%; Pred. No. 4,6e-194;  
Matches 775; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY	1	MSGGNIKVVVRVPRNAREIDRGACIVRMENQITLTPPPGAERKARKSGKTINDGPK 60		QY	61	AAFAFDRSYSPDKNAPNVAEROEDLPDGLVPLLDNAFKGYNCCIIFAYGOTGSGKSYSMWG 120	
DB	1	MSGGNIKVVVRVPRNAREIDRGACIVRMENQITLTPPPGAERKARKSGKTINDGPK 60		DB	61	AAFAFDRSYSPDKNAPNVAEROEDLPDGLVPLLDNAFKGYNCCIIFAYGOTGSGKSYSMWG 120	
QY	121	YGEHGVIRICODMFRRIINELOKDKNLTCYVAVSYLLEIYNEVRDLNLPSTYGNLKVRB 180		QY	121	YGEHGVIRICODMFRRIINELOKDKNLTCYVAVSYLLEIYNEVRDLNLPSTYGNLKVRB 180	
DB	121	YGEHGVIRICODMFRRIINELOKDKNLTCYVAVSYLLEIYNEVRDLNLPSTYGNLKVRB 180		DB	121	YGEHGVIRICODMFRRIINELOKDKNLTCYVAVSYLLEIYNEVRDLNLPSTYGNLKVRB 180	

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QY 181 HPSTGYVEDLAKLVVRSFOEINLMDENGNKARTVAATNMNETSRSRAVFTLTTLQKMH 240
DB 181 HSTSTGYVEDLAKLVVRSFOEINLMDENGNKARTVAATNMNETSRSRAVFTLTTLQKMH 240
QY 241 DEETKMDTEKVKAKISLVDLAAGERATSTGATGARLKEGAINEINSLTGLRVIAALADMSS 300
DB 241 DEETKMDTEKVKAKISLVDLAAGERATSTGATGARLKEGAINEINSLTGLRVIAALADMSS 300
QY 301 GKOQKQVLVPRYSVLTWLLKOSLGNSMTAMIAISPADINEEFTLSTRYVDSAKRIK 360
DB 301 GKOQKQVLVPRYSVLTWLLKOSLGNSMTAMIAISPADINEEFTLSTRYVDSAKRIK 360
QY 361 NHAVNEDPNARMIRELKEELAQLRSKLQSSGGGGAGAGSGGPVESEYPPDTPLEKOIV 420
DB 361 NHAVNEDPNARMIRELKEELAQLRSKLQSSGGGGAGAGSGGPVESEYPPDTPLEKOIV 420
QY 421 STQOPDPAVKKSKAEIVBOLNOSSEKLYRDNLQWEEKLAKTEEIHKEERAALEELGISI 480
DB 421 STQOPDPAVKKSKAEIVBOLNOSSEKLYRDNLQWEEKLAKTEEIHKEERAALEELGISI 480
QY 481 EKGFPVPRYSKEMPHLVNLSDDPLAECLVYNIKPGOTRGNVNOPTQAEIRLNGSKILK 540
DB 481 EKGFPVPRYSKEMPHLVNLSDDPLAECLVYNIKPGOTRGNVNOPTQAEIRLNGSKILK 540
QY 541 ECHTEFNVDNVTVIVNEKAAVWVNGVRIDKPTRLSGYRIILGDPHIFRNHPEERABE 600
DB 541 ECHTEFNVDNVTVIVNEKAAVWVNGVRIDKPTRLSGYRIILGDPHIFRNHPEERABE 600
QY 601 ROEOQLLRHSVTNSQLGSPAPGRHDTLSKAGSDADGDSRSDSPHPFGKSDWIFYARR 660
DB 601 ROEOQLLRHSVTNSQLGSPAPGRHDTLSKAGSDADGDSRSDSPHPFGKSDWIFYARR 660
QY 661 EASASALIGDOKISHLTDELALFPDVKARAVRGVLEDNDSOSQSPFRDXYMSN 720
DB 661 EASASALIGDOKISHLTDELALFPDVKARAVRGVLEDNDSOSQSPFRDXYMSN 720
QY 721 GTIDNFSLDTALTPTGTPRSDDGDLAFLFGDKSKODASVNDVEELRQOQAOMEALAKTA 780
DB 721 GTIDNFSLDTALTPTGTPRSDDGDLAFLFGDKSKODASVNDVEELRQOQAOMEALAKTA 780
QY 781 KOBF 784
DB 781 KOBF 784
QY 781 KOBF 784
DB 781 KOBF 784

RESULT 2
Q4X048_ASPFU PRELIMINARY; PRT; 1632 AA.
ID Q4X048_ASPFU
AC Q4X048;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-MAR-2006, entry version 6.
DE Kinesin family protein.
GN ORFNames=Alt291.4730;
OS Aspergillus fumigatus (Sartorya fumigata).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OC NCBI_TaxId=5085;
RN [1]
NC NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=AF293 / CBS 101355 / FGSC A1100;
RX PubMed=16372009; DOI=10.1038/nature04332;
NI Nierman W.C., Pain A., Anderson M.J., Mortman J.R., Kim H.S.,
AR Arroyo J., Bertman M., Abe K., Archer D.B., Bermejo C., Bennett J.W.,
BA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
BB Farman N., Fedorova N., Fedorova N.D., Feldblyum T.V., Fischer R.,
BC Fisman G.H., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
BD Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.J.,
BE Haas H., Harris D.E., Horluchi H., Huang J., Humphrey S., Jimenez J.,
BF Keller N., Khouri H., Kitamoto K., Kobayashi T., Konzack S.,
BG Kularni R., Kumagai T., Lafon A., Latge J.-P., Li W., Lord A.,
BH Lu C., Majores W.H., May G.S., Miller B.L., Mohamoud Y., Molina M.,
BI Monod M., Mouyna I., Mulligan S., Murphy L.D., O'Neill S., Paulsen I.,
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RA Penativa M.A., Perlea M., Price C., Pritchard B.L., Quail M.A.,
RA Rabinowitsch E., Rawlins N., Rajandream M.A., Reichard U.,
RA Renaud H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
RA Roming C.M., Ruter S., Salzberg S.L., Sanchez M.,
RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
RA Tacheichi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,
RA White O., Woodward J.R., Yu J.-H., Fraser C.M., Galagan J.E., Arai K.,
RA Machida M., Hall N., Barrell B.G., Denning D.W.;
RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
RT Aspergillus fumigatus."
RL Nature 438:1151-1156(2005).
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC -----
DR EMBL; AAH01000001; EAL93767.1; -; Genomic DNA.
DR GO; GO:005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:007018; F:microtubule-based movement; IEA.
DR InterPro; IPR001752; Kinesin_motor.
DR InterPro; IPR01849; PH.
DR InterPro; IPR01993; PH_type.
DR Pfam; PF00498; FHA; 1.
DR Pfam; PF00225; Kinesin; 1.
DR Pfam; PF00169; PH; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR SMART; SM00233; PH; 1.
DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE; PS00067; KINESIN_MOTOR_DOMAIN2; 1.
DR PROSITE; PS50003; PH_DOMAIN1; 1.
KW Complete proteome.
SQ SEQUENCE 1632 AA; 182726 MW; 1CAED6825E7744AD CRC64;

Query Match 79.8%; Score 3216; DB 2; Length 1632;
Best Local Similarity 78.6%; Pred. No. 2.5e-155;
Matches 636; Conservative 68; Mismatches 73; Indels 33; Gaps 8;

QY 3 CGGNIKVVRVRFNAREIDRGAKCIVMEGNQTLITPPGAEBARKS-GKTINDGPKA 61
DB 5 GGGNIKVVVRVRFNAREIDRGAKCIVMKNGTLLVPPGADKSRKAGGAVGEPKT 64
QY 62 PAPDRSYWSPDKAANRYARQEDLPDGLGVPLIDNAFKGYNNCTIYAGQTSKSKSYSMNGY 121
DB 65 PAPDRSYWSPDKAANRYARQEDLPDGLGVPLIDNAFKGYNNCTIYAGQTSKSKSYSMNGY 124
QY 122 GKEHGVIPRICODMFRRLNELOKDKNLCTVSVYLEIYNERVRRLDLPSTGKLVKREH 181
DB 125 GKEYGVIPRICODMFRRLNELOKDKNLCTVSVYLEIYNERVRRLDLPSTGKLVKREH 184
QY 183 PSTGYVEDLAKLVVRSFOEINLMDENGNKARTVAATNMNETSRSRAVFTLTTLQKMH 241
DB 185 PSTGYVEDLAKLVVRSFOEINLMDENGNKARTVAATNMNETSRSRAVFTLTTLQKMH 244
QY 242 BETKMDTEKVKAKISLVDLAAGERATSTGATGARLKEGAINEINSLTGLRVIAALADMSSG 301
DB 245 BETKMDTEKVKAKISLVDLAAGERATSTGATGARLKEGAINEINSLTGLRVIAALADMSSG 304
QY 302 KOKKQVLVPRYSVLTWLLKOSLGNSMTAMIAISPADINEEFTLSTRYVDSAKRIK 361
DB 305 KOKKQVLVPRYSVLTWLLKOSLGNSMTAMIAISPADINEEFTLSTRYVDSAKRIK 364
QY 362 HAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGAGAGSGG-PVESEYPPDTPLEKOIV 420
DB 365 HAVVNEDPNARMIRELKEELAQLRSKLQSSGGGGAGAGSGG-PVESEYPPDTPLEKOIV 420
QY 421 STQOPDPAVKKSKAEIVBOLNOSSEKLYRDNLQWEEKLAKTEEIHKEERAALEELGISI 480
DB 421 STQOPDPAVKKSKAEIVBOLNOSSEKLYRDNLQWEEKLAKTEEIHKEERAALEELGISI 480
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QY 481 EKGFGVYSHKEMPHLVNLSDDPLLAECVYNIKPQTRVGNVQDTQAEIRLNGSKILK 540
D 481 EKGFGVSTPKMPHVLNLSDDPLLAECVYNIKPQTTGNGMGSHVEIRLNGSKILP 540
QY 541 ECHTFEENVNVVTVIVNEKAAMVNGVRIDKPTRLSGRYIIIGDPIHFRFNHPEARAE 600
D 541 NCHTFEENVNVVTVIVNEKAAMVNGVRIDKPKLKGSPFIILGDFHIFRFNHPEARAE 600
QY 601 ROESQLRHSVTNSQSGPAPGR-HDRTLKAGSDAGD-SRSDSLPHRFGKDSMFYA 658
D 601 RVEOSLRHSVTNSQSGPAPGRHDKPTKSTGSELDGSSRADSPVQAGGEADMFYA 660
QY 659 RREASAILGLDQKISHLTDELDALEFDYQKAAVARGLVENEDSDSSQSFPRDKYM 718
D 661 RREAVSAIIGDPH-ISMPPDELDALFEDYQKATRGVLENDSDSLSSFFVRDKM 719
QY 719 SNGTIDNFSLDTAITMPTGTPRSDDGDALFFGD-KKSKOD----- 757
D 720 SNGTIDNFSLDTAITMPTGTPGQGYDGEQNGSDFTLQARQDMQRHLDKKEPKKRLRI 779
QY 758 --ASNVDELROQAQMEALKTAKQEF 784
D 780 AEAASDQADDELRLKEKMEBALSTKEY 808

RESULT 3
OSAVY3_EMENT PRELIMINARY; PRT; 1630 AA.
ID OSAVY3;
AC OSAVY3;
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
DT 07-MAR-2006, sequence version 1.
DE Hypothetical protein.
GN ORFNames=AN7547.2;
OS Aspergillus nidulans FGSC A4.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=227321;
RN [1]
RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
RC STRAIN=FGSC 4;
RX PubMed=16372000; DOI=10.1038/nature04341;
RA Galagan J.E., Calvo S.E., Cuomo C., Ma L.-J., Wortman J.R.,
RA Batzoglou S., Lee S.-I., Bastenkmann M., Spevak C.C., Clutterbuck J.,
RA Kapitonov V., Jurka J., Scanzonchio C., Farman M., Butler J.,
RA Purcell S., Harris S., Braue G.H., Draht O., Busch S., Butler J.,
RA Boucher C., Goldman G.H., Bell-Pedersen D., Griffiths-Jones S.,
RA Dougan J.H., Yu J., Vilenken K., Pain A., Freitag M., Selker E.U.,
RA Archer D.B., Penalva M.A., Oakley B.R., Momany M., Tanaka T.,
RA Kumagai T., Asai K., Machida M., Nieman W.C., Denning D.W.,
RA Caddick M., Hynes M., Paolucci M., Fischer R., Miller B.L., Dyer P.S.,
RA Sachs M.S., Osmann S.A., Birren B.W.;
RT "Sequencing of Aspergillus nidulans and comparative analysis with A.
RT fumigatus and A. oryzae."
RL Nature 438:1105-1115(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
EMBL: AACD01000129; EAA62127.1; -; Genomic DNA.
DR GO: GO:0005875; C: microtubule associated complex; IEA.
DR GO: GO:0005524; F: ATP binding; IEA.
DR GO: GO:0003777; F: microtubule motor activity; IEA.
DR GO: GO:0007018; F: microtubule-based movement; IEA.
DR InterPro: IPR000253; FHA.
DR InterPro: IPR001752; Kinesin_motor.
DR InterPro: IPR001849; PH.
DR InterPro: IPR011993; PH_type.
DR Pfam: PF00498; FHA; 1.
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DR Pfam: PF00225; Kinesin; 1.
DR Pfam: PF00169; PH; 1.
DR PRINTS: PR00380; KINESINHAAY.
DR SMART: SM00129; KISC; 1.
DR SMART: SM00233; PH; 1.
DR PROSITE: PS00411; KINESIN MOTOR DOMAIN1; 1.
DR PROSITE: PS50067; KINESIN MOTOR DOMAIN2; 1.
DR PROSITE: PS50003; PH DOMAIN; 1.
KW Hypothetical protein_
SQ SEQUENCE 1630 AA; 182784 MW; 85AD0AF238645F9D CRC64;

Query Match 78.6%; Score 3168; DB 2; Length 1630;
Best Local Similarity 78.0%; Pred. No. 7; Le-153;
Matches 627; Conservative 73; Mismatches 78; Indels 26; Gaps 10;

QY 3 GGGNIKYVVRVVRPNNAEIRDKAKCTVRMEGNGQITLTPPGAEEKARKSG-KITMDGPKA 61
D 5 GGGNIKYVVRVVRPNNAEIRDKAKCTVOMDSQITLTPPGAEEKARKSGKKAABGPKT 64
QY 62 FAFDRSYWSPDKAPVYARQEDLFODLGVPLDNAPFGYNNCFAYGQTSQSGKSYMMGY 121
D 65 FAFDRSYWSPDKAPVYAGQDNLFSDGVPLDNAPFGYNNCFAYGQTSQSGKSYMMGY 124
QY 122 GKEHGYVPRICQDMFRINELQKKNLCTVEVSYLEIYNERVRLDLPSTKGNLKYREH 181
D 125 GKEVGYVPRICQDMFRIRIKIQEDKTLCTVEVSYLEIYNERVRLDLPSTKGNLKYREH 184
QY 182 PSTGPYVEDLAKLVRSFOEINLMDGKARTVAATNNETSRSRAVFTLTLYOKMD 241
D 185 PSTGPYVEDLAKLVRSFEEINLMDGKARTVAATNNETSRSRAVFTLTLYOKMD 244
QY 242 EETKMTKVKAKTSLVDLGSERATSGARTGATLKGAEINRSLTIGRYIALADWSSG 301
D 245 AETSMDEKVSRLVDLGSERANSTGATGATLKGAEINRSLTIGRYIALADWSSG 304
QY 302 KQKKNQLVPRYDSVLTWMLKDSLGNSMTMAIASPADINFEETLSTLRVYDASAKRIK 361
D 305 K-KKGQVPRYDSVLTWMLKDSLGNSMTMAIASPADINFEETLSTLRVYDASAKRIK 363
QY 362 HAVVNEPNAAMIRLEKEIQAURSKLQSSGGGGAQSGGAV-EEYPPDTPLEKQIV 420
D 364 HAVVNEPNAAMIRLEKEIQAURSKLQSSGGGGAQSGGAV-EEYPPDTPLEKQIV 423
QY 421 STQPPDPAVYKSKAIVQLNOSSEKLYKDLNQTWEKLAKEEIKERPAALEEGIST 480
D 424 STQPPDPAVYKSKAIVQLNOSSEKLYKDLNQTWEKLAKEEIKERPAALEEGIST 483
QY 481 EKGFGVYSHKEMPHLVNLSDDPLLAECVYNIKPQTRVGNVQDTQAEIRLNGSKILK 540
D 484 EKGFGVSTPKMPHVLNLSDDPLLAECVYNIKPQTTGNGMGSHVEIRLNGSKILP 543
QY 541 ECHTFEENVNVVTVIVNEKAAMVNGVRIDKPTRLSGRYIIIGDPIHFRFNHPEARAE 600
D 544 DHCKFEENVNVVTVIVNEKAAMVNGVRIDKPTRLSGRYIIIGDPIHFRFNHPEARAE 603
QY 601 ROESQLRHSVTNSQSGPAPGR-HDRTLKAGSDAGD-SRSDSLPHRFGKDSMFYA 658
D 604 RVEOSLRHSVTNSQSGPAPGRHDKPTKSTGSELDGSSRADSPVQAGGEADMFYA 662
QY 659 RREASAILGLD-QKISHLTDELDALEFDYQKAAVARGLVENEDSDSSQSFPRDKY 717
D 663 RREAVSAIIGDPH-ISMPPDELDALFEDYQKATRGVLENDSDSLSSFFVRDKY 720
QY 718 MSNGTIDNFSLDTAITMPTGTPRSDDGDAL-----FGDKKSKODAS-N 760
D 721 MSNGTIDNFSLDTAITMPTGTPRHGDEDATLQSVQDMQRHLERQKQYIDKLRRESASP 780
QY 761 VVVEELRQQAQMEALKTAKQEF 784
D 781 QGIDELRSEKARMEDALRVAKKEY 804

RESULT 4
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 CC EMBL: AY330444; AA059306.1; -; Genomic\_DNA.  
 DR HSSP: P33173; 1155.  
 DR GO: GO:0005874; C:microtubule; IEA.  
 DR GO: GO:0005875; C:microtubule associated complex; IEA.  
 DR GO: GO:0005524; F:ATP binding; IEA.  
 DR GO: GO:0003777; F:microtubule motor activity; IEA.  
 DR GO: GO:0000166; F:nucleotide binding; IEA.  
 DR GO: GO:0007018; F:microtubule-based movement; IEA.  
 DR InterPro: IPR000253; FHA.  
 DR InterPro: IPR001752; kinesin\_motor.  
 DR Pfam: PF00498; FHA; 1.  
 DR Pfam: PF00225; kinesin; 1.  
 DR PRINTS: PRO0380; KINESINHEAVY.  
 DR SMART: SM00129; KISC; 1.  
 DR PROSITE: PS00411; KINESIN MOTOR DOMAIN1; 1.  
 DR PROSITE: PS50067; KINESIN MOTOR DOMAIN2; 1.  
 DR ATP-binding; Microtubule; Motor protein; Nucleotide-binding.  
 KM SEQUENCE 1087 AA; 120899 MW; B8F19ADB309E4D5 CRC64;  
 SQ  
 Query Match 69.8%; Score 2814.5; DB 2; Length 1087;  
 Best Local Similarity 70.3%; Pred. No. 4.6e-135;  
 Matches 575; Conservative 82; Mismatches 112; Indels 49; Gaps 14;  
 QY 2 SGGGNKKVVVVRVPPNAREIDRGAKCIYRMENQITITPPGABEKARKSGKTIIMGPKA 61  
 DB 4 TGGGNNKKVVVRCPSPNSREIERAKCIYEMKGNQTVTAEG--KGVKGG-----GPKA 55  
 QY 62 FAFDRSYWSPFDKAPNVAPOEDLFDLGVPLLDNAFKNYNCIFAYGQTSGSKSYSMGX 121  
 DB 56 FAFDRSYWSPFNKDDPNVAGSNLFDLGGPLLDNAFQYNNCFAYGQTSGSKSYSMGX 115  
 QY 122 GKSHGVIPIRCQMFRIINELQKDKLCTVEVSYLEYINERVRDLINPSTKGNLKYREH 181  
 DB 116 GKSHGIVPLICQMFRIIDELKDKLCTVEVSYLEYINERVRDLINPSTKGNLKYREH 175  
 QY 182 PSTGPIVVEDAKLVVVSFOEINLMDGNGKAFVATNNMSTSSRSRAVFTLLTQKMD 241  
 DB 176 PSTGPIVVEDAKLVVVSFOEINLMDGNGKAFVATNNMSTSSRSRAVFTLLTQKMD 235  
 QY 242 EETKMDTEKAKISLVDLGSEKATSGATGARKKEGAEINRSLSLSTGRVIAALADMSG 301  
 DB 236 ADTKMEMEKAKISLVDLGSEKATSGATGARKKEGAEINRSLSLSTGRVIAALADMSG 295  
 QY 302 KQKRNQ--VPRYDSVLTWLLKQSLGNSNTAMIAISPADINFEETSLTRYADSARKI 359  
 DB 296 GKXKKGTVGPYRDSVLTWLLKQSLGNSNTAMIAVSPADINFEETSLTRYADSARKI 355  
 QY 360 KNNAAVNEPDNMAIIEIKELAEQLSKLQSSGGGGGAGSGGPGVPESTPPTPLEKQI 419  
 DB 356 KNNAAVNEPDNMAIIEIKELAEQLSKLQSSGGGGGAGSGGPGVPESTPPTPLEKQI 414  
 QY 420 VSIQPDATVKKMSKAEIVQLNQSEKLYRDLNQTEBEKLAETKEIHKEREALAEIGIS 479  
 DB 415 VSIQSDGVLTKKVSKAEIVQLNQSEKLYRDLNQTEBEKLAETKEIHKEREALAEIGIS 474  
 QY 480 IEKGFVGYHKKMPLVNLSDPDLAECLVYNIKPGQTRVGNV--NODTQAEIRLNGSK 537  
 DB 475 IEKGFVGYHKKMPLVNLSDPDLAECLVYNIKPGQTRVGNV--NODTQAEIRLNGSK 534  
 QY 538 ILEKHTTFENV--DNVYTIYNEKKAAMVNGVRIIDKTRLSRGYRIILGPHIRFNHPEP 596  
 DB 535 ILHDHCTFEHAPDGVLTLPSEKASVMIKRIITPESQHSIGYRIILGPHIRFNHPEP 594  
 QY 597 ARAERQ-----QSLRHSVTNSQL-----GSPAPG--RHDRTLKAGSDADGDSRDS 643  
 DB 595 ARAERAEVPERPGLRHGSTITAQQLADLRGSPSPRPCHERSFVRVSEFG--ISRPES 653  
 QY 644 PLPHFR--GSDSWFYARREAAKILGLDKISHLTDELDALFDYQKARAVRGLEVDN 702  
 DB 654 PSIFQSGRESDSLARREAAKILGLSDQVLTSLTDEIINALFEDVQARAAR---VNGR 710

QY 703 ED-SDSOSPVPVADKXMSNCTINDFSLDPAITMPTGRSDDDGAL----- 747  
 DB 711 EDGDDSESSYPIDKXTLSNCTMDNFSLDALTMPSTPKQGPDDRLKEVREELQNRLEKQ 770  
 QY 748 --FFGDKKSKODASNVDEELRQQAQAMEEALTAQOE 783  
 DB 771 KEQYQQLMSAEANVIEIKQEKYKMEALKEKED 808  
 RESULT 6  
 ID Q86ZB4\_BOTCI PRELIMINARY; PRT; 1814 AA.  
 AC Q86ZB4;  
 DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.  
 DT 01-JUN-2003, sequence version 1.  
 DT 07-FEB-2006, entry version 17.  
 DE kinesin.  
 GN Name=Klup8;  
 OS Botrytis cinerea (Noble rot fungus) (Botryotinia fuckeliana).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;  
 OC Helotiales; Sclerotiniaceae; Botryotinia.  
 OX NCBI\_TaxID=40559;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=2627967; PubMed=12742059; DOI=10.1016/S1087-1845(03)00022-7;  
 RA Schoen C.L., Aist J.R., Yoder O.C., Gillian Turgon B.;  
 RT "A complete inventory of fungal kinesins in representative filamentous  
 ascomycetes.";  
 RL Fungal Genet. Biol. 39:1-15(2003).  
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 CC EMBL: AY330422; AA059284.1; -; Genomic\_DNA.  
 DR HSSP: P33173; 1155.  
 DR GO: GO:0005875; C:microtubule associated complex; IEA.  
 DR GO: GO:0005524; F:ATP binding; IEA.  
 DR GO: GO:0003777; F:microtubule motor activity; IEA.  
 DR GO: GO:0007018; F:microtubule-based movement; IEA.  
 DR InterPro: IPR000253; FHA.  
 DR InterPro: IPR001752; kinesin\_motor.  
 DR InterPro: IPR001849; PH.  
 DR InterPro: IPR011993; PH\_type.  
 DR Pfam: PF00498; FHA; 1.  
 DR Pfam: PF00225; kinesin; 1.  
 DR PRINTS: PRO0380; KINESINHEAVY.  
 DR SMART: SM00129; KISC; 1.  
 DR PROSITE: PS00411; KINESIN MOTOR DOMAIN1; 1.  
 DR PROSITE: PS50067; KINESIN MOTOR DOMAIN2; 1.  
 DR PROSITE: PS50003; PH DOMAIN; 1.  
 SQ SEQUENCE 1814 AA; 201181 MW; 5F989F1BF2622BA1 CRC64;  
 Query Match 68.8%; Score 2773; DB 2; Length 1814;  
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 Matches 575; Conservative 63; Mismatches 105; Indels 48; Gaps 14;  
 QY 31 MEGNQITILPPGAEKAR--KSGKTIIMGPAPAFDRSYWSPFDKAPNVAPOEDLFDL 88  
 DB 1 MKDAQVITIRPPEGHEKSKDAKGKA--DTGQVAFAFDRSYWSPFDKNDPSYAGQDNILHTL 59  
 QY 89 GVPLLDNAPKGYNNCFIAYGQTSGSKSYSMGXGKSHGVIPIRCQMFRIINELQKDKL 148  
 DB 60 GVPLLDNAPKGYNNCFIAYGQTSGSKSYSMGXGKSHGVIPIRCQMFRIINELQKDKL 119  
 QY 149 TCTVEVSYLEYINERVRDLINPSTKGNLKYREHPSGPIVEDAKLVVVSFOEINLMD 208  
 DB 120 KCTVEVSYLEYINERVRDLINPSTKGNLKYREHPSGPIVEDAKLVVVSFOEINLMD 179  
 QY 209 GNKARTVAATNNMSTSSRSRAVFTLLTQKMDDEETKMDTEKAKISLVDLGSEKATSG 268  
 DB 180 GNKARTVAATNNMSTSSRSRAVFTLLTQKMDDEETKMDTEKAKISLVDLGSEKATSG 239

QY 269 GATGARKKEGAEINRSLSTLGRVIALALADMSCKOKK----NOLVPRDSVLTWLLKDSI 324  
 DB 240 GATGARKKEGAEINRSLSTLGRVIALALADMSCKKKKVKQKQ--VYRDSVLTWLLKDSI 298  
 QY 325 GGNSTMTAMIAISPADINFEETLSTLRVYDSAKRIQNHAVNDDPARMIRELKEELAOJ 384  
 DB 299 GGNSTMTAMIAISPADINFEETLSTLRVYDSAKRIQNHAVNDDPARMIRELKEELAOJ 358  
 QY 385 RSKLOSSGGGGGAGSGGSGPVESYPPDPLEKQIVSIOQPDATVKKMSKAEIVEOLNOS 444  
 DB 359 RSKLT--TGCGGWRGRGS--PADEIYAEAGTPELEKQMTIVISSDPAVKVSKAEITEOLNOS 414  
 QY 445 EKLTYDNLNTWEKLAKTETIHKEREALAEIGISTEKGPGYHSEKMPHVNISDDDL 504  
 DB 415 EKLTYDNLNTWEKLOKTEIHKEREALAEIGISTEKGPGYHSEKMPHVNISDDDL 474  
 QY 505 LAECLVYNNIKPGQTRVGNV--NQDTQAEIRLNGSKILKEHCTEENVDNVTVIPEKEAAV 562  
 DB 475 LAECLVYNNIKPGQSTVGNVDTNAHAAEIRLNCTRIHHECTEENVDNVTVIPEKEAAV 534  
 QY 563 MNGVRIDKPTRLRSQYRIILGDFHIFRPNHPEAPAEKQEOSLHSHVTSNQL----- 616  
 DB 535 MNGQREKPTRLRSQYRIILGDFHIFRPNHPEAPAEKQEOSLHSHVTSNQL----- 594  
 QY 617 -----GSPAPGRHDTLSKAGSDA--DDDSRSDSPLPHRGKDSMFYARPREAASAIIG 668  
 DB 595 DKFSPSSTPRPA-HDFTFSKAIISDLDFDSSRSDSVPFG-RGL-SWMSLARRRFAAGAILG 651  
 QY 669 LDQKISHLTDELDALFDVQKARAVRGVLVEDNEDSDSQSFPPVADKYMSNTGINDFSL 728  
 DB 652 TQOKTAGLSDEELNVLFEDVQARRA-ERAPTANLEDDLSTVTSYPMKEKTLNSNTLDNFSJ 710  
 QY 729 DTAITMPTGPRSDDDGAL-----FFGDKKSQKQDSNVDSVEILRQOQAO 772  
 DB 711 DTAITMPTGPRSGEVEDRMRKEVKEEMQVLEKOREBEFQDLIAKTSNVEBEIKKEKVR 770  
 QY 773 MEALAKTAKOE 783  
 DB 771 MEETLEKVEKE 781

## RESULT 7

Q4HXW9\_GIBZE PRELIMINARY; PRT; 1793 AA.  
 AC Q4HXW9; 16-AUG-2005, integrated into UniProtKB/TrEMBL.  
 DT 16-AUG-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 6.  
 DE Hypothetical protein.  
 GN ORFNames=FGI10189.1;  
 OS Gibberella zeae (Fusarium graminearum).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.  
 OX NCBI\_TaxID=5518;  
 RN NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).  
 RC STRAIN=PH-1 / NRRL 31084.  
 RA Birren B.W., Nusbaum C., Abouelleil A., Allen N., Anderson S.,  
 Archachal H.M., Barna N., Bastien V., Bloom T., Boguslavskiy L.,  
 Bouhaghel B., Butler J., Calvo S.E., Camarata J., Chang J.,  
 Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeRellano K.,  
 Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,  
 Eriksson J., Faro S., Ferreira P., FitzGerald M., Gage D.,  
 Galagan J.E., Gardyna S., Gierke S., Graham L., Grand-Pierre N.,  
 Hafez N., Hagopian D., Hagoeb B., Hall J., Horton L., Hulme W.,  
 Iliev I., Jaffe D., Johnson R., Jones C., Kamal M., Kanat A.,  
 Karczias A., Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G.,  
 Manning J., Matthews C., Mauceli E., McCarthy M., Melidrim J.,  
 Menus L., Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C.,  
 Nicol R., Nielsen C.B., Nordu K., O'Connor T., O'Donnell P.,  
 O'Neill D., Oliver J., Peterson K., Phunkhang P., Pierre N.,

RA Purcell S., Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C.,  
 Rogov P., Roman J., Schuer S., Schupbach R., Seaman S., Severy P.,  
 Smitnov S., Smith C., Spencer B., Stange-Thomann N., Stojanovic N.,  
 RA Stubbs M., Talames J., Testaye S., Theodore J., Topham K., Travers M.,  
 RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,  
 RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,  
 RA Lander E.S.;  
 RT "Fusarium graminearum genome sequence."  
 RL Submitted (Feb-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
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 CC -----  
 DR EMBL; AAC001004.4; EAA70032.1; -; Genomic DNA.  
 DR GO; GO:0005875; C:microtubule associated complex; IEA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0003777; F:microtubule motor activity; IEA.  
 DR GO; GO:0007018; F:microtubule-based movement; IEA.  
 DR InterPro; IPR001752; Kinesin\_motor.  
 DR InterPro; IPR001849; PH.  
 DR Pfam; PF00498; FHA; 1.  
 DR Pfam; PF00225; Kinesin; 1.  
 DR Pfam; PF00169; PH; 1.  
 DR PRINTS; PR00380; KINESINHEAVY.  
 DR SMART; SM00129; KISC; 1.  
 DR SMART; SM00233; PH; 1.  
 DR PROSITE; PS00411; KINESIN\_MOTOR\_DOMAIN1; 1.  
 DR PROSITE; PS50067; KINESIN\_MOTOR\_DOMAIN2; 1.  
 DR PROSITE; PS50003; PH\_DOMAIN; 1.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 1793 AA; 198597 MW; 44AF342ED904207 CRC64;  
 Query Match 68.5%; Score 2761.5; DB 2; Length 1793;  
 Best Local Similarity 68.8%; Pred. No. 4,7e-132;  
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 QY 2 SGGGNIKYVYRVRPNARIBDGAQCIYRMESGNTITLPPFGAEKAKSKGTIND-GRK 60  
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 AGGGNIKVVRCRPNRSRIBRNACIYEMKGNQTVITAP-----EGGVNDGSRK 54  
 QY 61 AFAFDSYWSFDKMPNYPVAROEDLFQDGVPLLDNAFAGYNNCFAYGQTSKSGSKSYNMG 120  
 DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 55  
 AFAFDRSYSEFKDPPNVAAGSNLFDJGQPLDPAFEYNNCFAYGQTSKSGSKSYNMG 114  
 QY 121 YKEKGVIPRLICQDMFRRINELQDKNLCTYVESYLEIYNERVADLLNPSTKGLKYRE 180  
 DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 115  
 YKEIGIYVMICQEIFKADDEIQDKGKTKTYEVSYLEIYNERVADLLNPSTKGLKYRE 174  
 QY 181 HSTGTPYVEDLAKLVYRSFOETENLMDGKARKATVAAATNMETSRSRAVFTLTQKWH 240  
 DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 115  
 HSTGTPYVEDLAKLVNFOETENLMDGKARKATVAAATNMQTSRSRAVFTLTQKKI 234  
 QY 175 HSTGTPYVEDLAKLVNFOETENLMDGKARKATVAAATNMQTSRSRAVFTLTQKKI 234  
 DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 175  
 DEETQDTEKVAKISLVLDAGSERATSGATGARLKEGAETIRSLSTLGRVIALADMS 300  
 QY 241 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 241  
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 DB 235 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 235  
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 294  
 QY 301 -GKQKNO-LVPRDSVLTWLLKDSLGNSMTAMIAISPADINFEETLSTLRVYDSAKR 358  
 DB 295 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 295  
 PEKKKKSGSQVYRDSVLTWLLKDSLGNSMTAMIAISPADINFEETLSTLRVYDSAKR 354  
 QY 355 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 355  
 INHNVNVEDPARMIRELKEELSLRGLT---GGGGGPGGAVVAG---ETVAGTPI 407  
 DB 355 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 355  
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 QY 417 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 417  
 KOIVSIQPDATVKKMSKAEIVEQINQSEKLYRDNLQNTWEKLAKTETIHKEREALAE 476  
 DB 408 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 408  
 QMVSITGPDGVLKVVSAEIEQLSQSEKLLTDNLQNTWEKLAKTETIHKEREALAE 467  
 QY 477 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 477  
 GISIEKFGVGYHSEKMPHVNLSDDPLAECLVYNNIKPGQTRVGNV--NQDTQAEIRLN 534



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Db 468 GUSIEKGVGLHTPKKPHLVNLSDDPLAECLVNLKPGTTGVGNVDINADHOANIRLN 527
Qy 535 GSKILKEHCTFEN-VDNVVTIVNEKAAMVWNGVRIDKPTLRSGYRIILIGDPHIFRPNH 593
Db 528 GSKILHDHCSFEAAAGTTLTPSEBAGSVINIKRITPEQSLSGVRILGDPHIFRPNH 587
Qy 594 PEFAARAEORQ-----OSLRHSVTSNQL-----GSPAPG--RHDRTLSAGSDADGDSR 640
Db 588 PHEARAEARAEVPRPSQLRHSITASQLQLADRGSPSPSPRPGHERSFSRSEFGD-ISR 646
Qy 641 SOSPLPHFR-GKSDMPFYARREASAILGDKIKSHLTDELDLALPDVQKAAVNRGLV 639
Db 647 PEPSPFQNRGRSSDLSARREAGAILGSDQNLTSLSDELNALFEDEVQKAAERVNR 706
Qy 700 EDNEDSDSQSPFVRDKYMSNGTIDNPSLDTAITMPTGTPSPDDGDAL----- 747
Db 707 EDGDDSD--SYIRKRYLSNGTMDNPSLDTALTMSTPKQGEPRDRLRVRRELQNKLE 764
Qy 748 ---PFGDKSKQDASNVDEELRQQAQMEALKTAKOE 783
Db 765 KQKEEVQDQLKSAAANVEIEIKQEKVKEALQELKED 804

RESULT 8
Q86Z3 COCHE PRELIMINARY; PRT; 1666 AA.
ID Q86Z3 COCHE
AC Q86Z3
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE Kinesin.
GN Name=KLP8;
OS Cochliobolus heterostrophus (Drechslera maydis).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Cochliobolus.
OX NCBI_TaxID=5016;
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22627967; Pubmed=12742059; DOI=10.1016/S1087-1845(03)00022-7;
RX Schoch C.L., Aist J.R., Yoder O.C., Gillian Turgeson B.,
RT "A complete inventory of fungal kinesins in representative filamentous
RL ascomycetes.";
RL Fungal Genet. Biol. 39:1-15(2003).
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CC -----
CC EMBL; AY230433; AA059295.1; -; Genomic_DNA.
DR HSSP; P33173; 1158.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; F:microtubule-based movement; IEA.
DR InterPro; IPR001842; FHA.
DR InterPro; IPR001752; kinesin_motor.
DR InterPro; IPR011849; PH.
DR InterPro; IPR011993; PH_type.
DR Pfam; PF00498; FHA; 1.
DR Pfam; PF00225; kinesin; 1.
DR Pfam; PF00169; PH; 1.
DR PRINTS; PRO0380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN MOTOR DOMAIN; 1.
DR PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
DR PROSITE; PS50003; PH DOMAIN; 1.
SQ SEQUENCE 1666 AA; 186129 MM; 9F58CCCCCF80F16EA CRC64;

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Qy 91 PLIDNAFKYNNICIFAYGOTSGSKSYMMGYGEHGVIPRICODMFRRIINELQDKNLTG 150
Db 124 PLIDNAFQGINNICIFAYGOTSGSKSYMMGYGEHGVIPRICODMFRRIINELQDKNLTG 163
Qy 151 TVEVSYLEIYNERVRDLNLPSTKGNLKVREHPSTGPVEDLAKLVRSFOEINLDEGN 210
Db 184 TVEVSYLEIYNERVRDLNLPSTKGNLKVREHPSTGPVEDLAKLVRSFOEINLDEGN 243
Qy 211 KATVAATMNETSSSHAVFTLTQKHDEETKQDTEKVAKISLYDLAGEBATSTGA 270
Db 244 KATVAATMNETSSSHAVFTLTQKHDEETKQDTEKVAKISLYDLAGEBATSTGA 303
Qy 271 TGAIRKEGAEINRSLTGRVITAAALDMSGKKKNQVLYRPSVLTWILKDSLGNSMT 330
Db 304 TGAIRKEGAEINRSLTGRVITAAALDMSGKKKAQ-VPRDSILTLTKDLSLGNSMT 361
Qy 331 AMIAAISPADINFEETLSTLRVADSARKIKNAHVNEDPNARMIRELKEBLAQLRSKLG 390
Db 362 AMIAAISPADINFEETLSTLRVADSARKIKNAHVNEDPNARMIRELKEBLAQLRSKLG 421
Qy 391 SGGGGGAGSGGSGVPEESTPPTPLEKQIVSIQDPATVKKSKAEIVBOLNSEKLYRD 450
Db 422 GGGGGGAGSGSGNGIVEQYPPDTPLEKQWVSITQADGSTKYSKAEIAEQLTQSEKLYTE 481
Qy 451 LNTQWEKLAKTEIHKEREAALAEIGISIEKGFPVGRPHYSKEMPHLVNSDDPLAECLV 510
Db 482 LNTQWEKLQKTEIHKEREAALAEIGISIEKFPVLSPPKMPHVLNLSDDPLAECLV 541
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Db 542 YNKPQTRGVNNOPTQ-AEIRLNGSKILKEHCTFENVNVTIVNEKAAMVWNGVR 601
Qy 570 DKPTLRSGYRIILGDPHIFRPNHPEARAEORQ-OsLRHSVTSNQLGS-----PAPG 622
Db 602 DKPTLRSGYRIILGDPHIFRPNHPEARAEORQ-OsLRHSVTSNQLGS-----PAPG 661
Qy 623 RHRH---TISKAGSDADGGS-RSDSPLPHFRGDSQMFYARRAASAILGDKIKSHLTPD 678
Db 662 -HRSYSISIVANSDDPSPFRAGSPALWQGRSESFSAARRALTAWLPDRRIEPLD 720
Qy 679 DELDALFDVQKAAVARG-----LVEDNEDSDSQSPFVRDKYMSNGTIDNPSLDTAIT 723
Db 721 EDPEALYEDLSRLRETRKARPESSMTSDGDTSMNSYPRREKXAGGTLIDNPSLDTALT 780
Qy 734 MPTGTPSD-----DDGDLFPFGDKSKQDASNVDEELRQQAQOM 773
Db 781 MPTGTPSD-----DDGDLFPFGDKSKQDASNVDEELRQQAQOM 835
Qy 774 EELAKTAKQEF 784
Db 836 QRMQKAKQEA 846

RESULT 9
Q2UE08 ASPOR PRELIMINARY; PRT; 1519 AA.
ID Q2UE08 ASPOR
AC Q2UE08
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 3.
DE Kinesin-like protein.
GN ORFNames=AO090026000806;
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=RIB 40;
RX Pubmed=16372010; DOI=10.1038/nature04300;

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RA Machida M., Arai K., Sano M., Tanaka T., Kumagai T., Terai G.,  
 RA Kusumoto K., Arima T., Akita O., Kashiwagi Y., Abe K., Gomi K.,  
 RA Horikuchi H., Kitamoto K., Kobayashi T., Takeuchi M., Denning D.W.,  
 RA Galagan J.E., Nierman W.C., Yu J., Archer D.B., Bennett J.W.,  
 RA Bhattacharjee D., Cleveland T.E., Fedorova N.D., Gotoh O., Hotikawa H.,  
 RA Hosoyama A., Ichinomiya M., Igasaki R., Iwashita K., Juvvadi P.R.,  
 RA Kato M., Kato Y., Kim T., Kokubun A., Maeda H., Maekawa N.,  
 RA Maruyama J., Nagasaki H., Nakajima T., Oda K., Okada K., Paulsen I.,  
 RA Sakemoto K., Sawano T., Takahashi M., Takase K., Terabayashi Y.,  
 RA Wortman J.R., Yamada O., Yamagata Y., Anazawa H., Hata Y., Koide Y.,  
 RA Komori T., Koyama Y., Minetoki T., Sunahara S., Tanaka A., Isono K.,  
 RA Kishimoto S., Ogasawara N., Kikuchi H.;  
 RA "Genome sequencing and analysis of *Aspergillus oryzae*.";  
 RL Nature 438:1157-1161(2005).  
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 CC EMBL, AP007159; BAE60207.1; -; Genomic DNA.  
 DR SEQUENCE 1519 AA; 169635 MW; FOA56250F5859B6 CRC64;

Query Match 65.4%; Score 2634; DB 2; Length 1519;  
 Best Local Similarity 67.7%; Pred. No. 1,2e-125;

Matches 536; Conservative 58; Mismatches 68; Indels 130; Gaps 9;

3 GGGATKVVVRVPPNAREIDRGACIVRMENQITLPPGAEEKARKS--GKTIWDGPK 60  
 5 GGGATKVVVRVPPNAREIDRGACIVRMENQITLPPGAEEKARKS--GKTIWDGPK 64  
 61 AFAFDRSYWSPDKNAFVYVQEDLFDGLVPLLDNAFKYNNCFYVGGTSGSKYSWMG 120  
 65 TFAFDRSYWSPDKNAFVYVQEDLFDGLVPLLDNAFKYNNCFYVGGTSGSKYSWMG 124  
 121 YGKEGVIPRIQODMFRINELQKDNLTCTVEVSLTYNERYVRLLPSTGNLKARE 180  
 125 YGKEGVIPRIQODMFRINELQKDNLTCTVEVSLTYNERYVRLLPSTGNLKARE 184  
 181 HPSSTPYVEDLAKLVRSFOEIEMLDEGNKARTVATNMNETSRSRHVFTLTLOKMH 240  
 185 HPSSTPYVEDLAKLVRSFOEIEMLDEGNKARTVATNMNETSRSRHVFTLTLOKMH 244  
 241 DEETMDTEKVAKISLVLDAGSERATSGATGARLKEGAINRSLSLTGRVIAALDMS 300  
 245 DAETMDTEKVAKISLVLDAGSERATSGATGARLKEGAINRSLSLTGRVIAALDMS 304  
 301 GQOKKQVLPYRDSVLTWLLKSLGNSMTAMIAISPADINPEETLSTRYADSKRIK 360  
 305 GQKQASWVPYRDSVLTWLLKSLGNSMTAMIAISPADINPEETLSTRYADSKRIK 364  
 361 NHAIVNEDNARMIRELKEELAQRLSKLQSSGGG---GGAGS---GGPYEESYPPD 412  
 365 NHAIVNEDNARMIRELKEELAQRLSKLQSSGGG---GGAGS---GGPYEESYPPD 420  
 413 TPLEKQIVSIQOPDATVKKMSKAEIYEQUNOSEKLYRDINQWEEKLATEEIHKEEA 472  
 421 TPLEKQIVSIQOPDATVKKMSKAEIYEQUNOSEKLYRDINQWEEKLATEEIHKEEA 480  
 473 LBEELGISIEKGVGPRHAKEMPHLVNLSDDPLLAELVYNIRGQRRVGNVADTAEIR 532  
 481 LBEELGISIEKGVGPRHAKEMPHLVNLSDDPLLAELVYNIRGQRRVGNVADTAEIR 540  
 533 LNSGKILKHCETFEVDNVVTIVPNEKAVVMVNGVVIDPTRLRSRGYIILGPFHFRN 592  
 541 LNSGKILKHCETFEVDNVVTIVPNEKAVVMVNGVVIDPTRLRSRGYIILGPFHFRN 600  
 593 HPEEARAEQEOSLLRHVSNTSOLGSPABGRDRTLKAGSDADGDSRSDPLPHFRGKD 652  
 601 HPEEARAEQEOSLLRHVSNTSOLGSPABGRDRTLKAGSDADGDSRSDPLPHFRGKD 656  
 653 SDWFAARRAASAILGLDOKISHLTDELDALFDVYQKRAVARGIIVEDNEDSDSSSFP 712  
 657 SDWFAARRAASAILGLDOKISHLTDELDALFDVYQKRAVARGIIVEDNEDSDSSSFP 712

QY 713 VDKTWSNCTIDNFSLDIAITMGPTRSDDDGALFEDGKSKQDASNVDEELRQOQA 772  
 DB 644 LNNALSSQO-----GVENHSEKAR 664  
 QY 773 MEALAKTAKEF 784  
 DB 665 MEALAKTAKEF 676

RESULT 10  
 ID Q4P0W2\_USTMA PRELIMINARY; PRT; 1676 AA.  
 AC Q4P0W2;  
 DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.  
 DT 19-JUL-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 7.  
 DE Hypothetical protein.  
 GN ORFNames=DM06251.1;  
 OS Ustilago maydis 521.  
 OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;  
 OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.  
 NC NCBI\_TaxId=237631;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=521;  
 RA Birren B.W., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,  
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 RA Arachchi H.M., Armbruster J., Bachantsang P., Baldwin J., Barry A.,  
 RA Bayul T., Biletscheyn B., Bloom T., Biye J., Boguslavskiy L.,  
 RA Borowsky M., Boukngalter B., Brunache A., Butler J., Calixte N.,  
 RA Calvo S.E., Camarata J., Campo K., Chang J., Cheshtsang Y.,  
 RA Citroen M., Collamore A., Considine T., Cook A., Cooke P., Corum B.,  
 RA Cuomo C., David R., Dawoe T., Degray S., Dodge S., Doolley K.,  
 RA Dorje P., Dorjee K., Dorris L., Dufey N., Dupes A., Ekins T.,  
 RA Engels R., Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,  
 RA Fitzgerald M., Foley K., Gage D., Galagan J.E., Gealrin G., Gierre S.,  
 RA Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltzen K., Hafez N.,  
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 RA Lindblad-Toh K., Liu X., Lokysang T., Lokysang Y., Lucien O.,  
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 RA Manning J., Marbella R., Maru K., Matthews C., Mauceli E.,  
 RA McCarthy M., McDonough S., McChae T., Meldrum J., Meneses L.,  
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 RA Mozes J., Mulrain L., Munson G., Naylor J., News C., Nguyen C.,  
 RA Nguyen N., Nguyen T., Nicol R., Nielsen C.B., Nizzari M., Norbu C.,  
 RA Norbu N., O'Donnell P., Okaso O., O'Leary S., Omotosho B.,  
 RA O'Neill K., Oman S., Parker S., Perrin D., Phunkhang P., Piganl B.,  
 RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,  
 RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,  
 RA Rutman M., Schnupbach R., Seaman C., Settipalli S., Sharpe T.,  
 RA Spencer B., Stalker J., Stange-Thomann N., Stavropoulos S.,  
 RA Stelson K., Stone C., Stone S., Stubbs M., Talmas J., Tchunga P.,  
 RA Tenzing P., Tesfaye S., Theodore J., Thoulissang Y., Topham K.,  
 RA Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H., Wang X.,  
 RA Venkataraman V.S., Vanshon J., Vo A., Wade C., Wang S., Wangchuk T.,  
 RA Wandi T., Whitaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,  
 RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,  
 RA Zimmer A., Zody M., Zander E.S.;

RT "The genome sequence of *Ustilago maydis*."  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.

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 CC Distributed under the Creative Commons Attribution-NonDerivs License  
 CC EMBL, AACP01000237; EAK87131.1; -; Genomic DNA.

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DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro: IPR000253; FHA.
DR InterPro: IPR001752; kinesin_motor.
DR InterPro: IPR001849; PH.
DR Pfam: PF00498; FHA; 1.
DR Pfam: PF00225; kinesin; 1.
DR Pfam: PF00169; PH; 1.
DR PRINTS; PRO0380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR SMART; SM00233; PH; 1.
DR PROSITE; PS50006; FHA DOMAIN; 1.
DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
DR PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR Hypothetical protein.
KW SEQUENCE 1676 AA; 184606 MW; A44A5CD7B2EA99AE CRC64;

Query Match      48.6%; Score 1957.5; DB 2; Length 1676;
Best Local Similarity 51.8%; Pred. No. 4.9e-91;
Matches 426; Conservative 111; Mismatches 194; Indels 91; Gaps 19;

QY 1 MSGGNIKVVVRVPRPNAREIDRGACIVR-MEGNQTILTPPGAEKARKSGKTIIDGP 59
DB 1 MDSGNIKVVVRCRPNRSRRNRGASNLIEFVDQHLLSPNEADTK--ENSKATKKKS 58
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DB 59 MPFSFPRAY-----DEHTEODDLFOYIGVELLOHAFNGFNTCVFAYGQTSGSKSHSV 111
QY 120 GYKGEHGVPRICQDMFRINE-LQDKKNLTCTVEVSYEIYNERVRLDLPSTKGNLKY 178
DB 112 GYAQAGIILPLTCARLFEDINQKTADPNLKISVEVSYEIYNEKVRDLNPNKGNLKY 171
QY 179 REHPSGTPEYEDLAKLVRSFOEINLMDGKARTVAATNNNETSSRSRAVFTLTQK 238
DB 172 REHPSLGPVEYEDSLKLVASYPDINMLMDGKARTVAATNNNETSSRSRAVFTLTQK 231
QY 239 WHDEFKMDTEKAKISLVDLAGEPATSTGATGARLKEGAEINRSLSLTGRVIAIADM 298
DB 232 RPDVQTKLEAEKYSRISMVDLAGSERANSTGATGARLKEGANINRSLSLTGKVIALLAIA 291
QY 299 SS-----GKOKK-----NQLVPRDSVLTWLLKDSLGSMSMTAMIAISPADINEETL 347
DB 292 SSABVEPKAKKPKTASLDSFVPRDSVLTWLLKDSLGSMSMTAMIAISPAD--YEETL 349
QY 348 STLRYADSAKRIKNAHVVEDPNARMIRLKEELAQLRSLQSSGGGGGAGSGGPVEE 407
DB 350 STLRYADQAKKIKNAHVVEDPNAKIRLKELELLRTRV---SGGGGAGD-----BS 400
QY 408 STPPTPLEKQIVSIQOPDATVYKMSKAEIVELQNLSEKLYRDLNQTWEKLAKEEIHK 467
DB 401 NNDPSIPDPKQVRYQTGTGEIKTVTKAELOEQSEKIMSLNSMSEKLTKEIQIK 460
QY 468 EREAALEELGISTEKEFGVPRYHSEKMPHLVNSDDLLAECLVYNIKKPGOTRGANNQDT 527
DB 461 EREKALEELGISTVDKNVGHVTPKPLPHLVNLMEDPLMECLLYQIKPGTTLVGNLDSGP 520
QY 528 QAEIRLNGSKILKEHTCFENVDNVVTIVPNEKAAVNVNGVRI--DKPTRLRSGYRIILGD 585
DB 521 DVHILKSGRIKLNKCMFHQDGLVYVTAMPDSMTMVNKGRLAPDPKRLRSRYRIILGD 580
QY 586 FHIIPRNPPEBAERFQEOSLLRHSVTNSQLSPAPGRDRTLKSKASDADG--SRAD 642
DB 581 FHVFRNHEBEVYKADR-----VRSTLALSTGEAHNETL-----IDGLPSTRPD 626
QY 643 SPLPHRGSDQWVFYAREAAAIL-GLDQKISHLDDDELDAFDVYOKARA----- 693
DB 627 SP---ASGDVDPYTTARREYTAKLNGQVNVNFDNLDELEKLFEDIISRAKSKSGSVL 682
QY 694 ----VARGLVEDNEDEDSQSFPVRDKYNSNGTIDNFSLDATITMGTGTPRSDDDGDLFF 749

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DB 683 GRPESRASFEDDNA-----SEASASSVIRYSHGALTDPTSID-----PWSQAGSEWGRFS 734
QY 750 GDKKSQOD-----ASNVDVELRQOQAOAMEAL 777
DB 735 AGPIKENAYTGAGASPALVAASHRETESLRAKVREYBEKL 776

RESULT 11
ID Q8TG36_USTMA PRELIMINARY; PRT; 1676 AA.
AC Q8TG36;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE kinesin.
GN Name=kln3;
OS Ustilago maydis (Smut fungus).
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OX NCBI_TaxID=5270;
RN [1]
RP NCLEOTIDE SEQUENCE.
RX MEDLINE=22060494; PubMed=12065408; DOI=10.1093/emboj/cdf296;
RA Medlich-Solander R., Straube A., Friedrich M.W., Steinberg G.;
RT "A balance of Kif1a-like kinesin and dynein organizes early endosomes
in the fungus Ustilago maydis."
EMBO J. 21:2946-2957(2002).
CC -----
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CC distributed under the Creative Commons Attribution-NonDerivative License
CC -----
DR EMBL; AF480446; AL487137.1; -; Genomic_DNA.
DR HSP; P33173; 1161.
DR GO; GO:0005875; C:microtubule associated complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003777; F:microtubule motor activity; IEA.
DR GO; GO:0007018; P:microtubule-based movement; IEA.
DR InterPro: IPR000253; FHA.
DR InterPro: IPR001752; kinesin_motor.
DR InterPro: IPR001849; PH.
DR InterPro: IPR011993; PH_type.
DR Pfam; PF00498; FHA; 1.
DR Pfam; PF00225; kinesin; 1.
DR Pfam; PF00169; PH; 1.
DR PRINTS; PRO0380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR SMART; SM00233; PH; 1.
DR PROSITE; PS50006; FHA DOMAIN; 1.
DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
DR PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
SQ SEQUENCE 1676 AA; 184606 MW; A44A5CD7B2EA99AE CRC64;

Query Match      48.6%; Score 1957.5; DB 2; Length 1676;
Best Local Similarity 51.8%; Pred. No. 4.9e-91;
Matches 426; Conservative 111; Mismatches 194; Indels 91; Gaps 19;

QY 1 MSGGNIKVVVRVPRPNAREIDRGACIVR-MEGNQTILTPPGAEKARKSGKTIIDGP 59
DB 1 MDSGNIKVVVRCRPNRSRRNRGASNLIEFVDQHLLSPNEADTK--ENSKATKKKS 58
QY 60 KAFAPFRSTWSFPMKAPNARQEDLFQDLCVPLLDNAFPGYNNCTAYAGQTSGSKSYSMM 119
DB 59 MPFSFPRAY-----DEHTEODDLFOYIGVELLOHAFNGFNTCVFAYGQTSGSKSHSV 111
QY 120 GYKGEHGVPRICQDMFRINE-LQDKKNLTCTVEVSYEIYNERVRLDLPSTKGNLKY 178
DB 112 GYAQAGIILPLTCARLFEDINQKTADPNLKISVEVSYEIYNEKVRDLNPNKGNLKY 171
QY 179 REHPSGTPEYEDLAKLVRSFOEINLMDGKARTVAATNNNETSSRSRAVFTLTQK 238
DB 172 REHPSLGPVEYEDSLKLVASYPDINMLMDGKARTVAATNNNETSSRSRAVFTLTQK 231

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[illegible]

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RESULT 12
055Z46.CRYNE
ID 055Z46.CRYNE PRELIMINARY; PRT: 1556 AA.
AC 055Z46;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Hypothetical protein.
GN ORNameaB=CNBA6420;
OS Cryptococcus neoformans var. neoformans B-3501A.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxId=283643;
[]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=B-3501A;
RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
RA Wickes B.L., Fu J., Davis R.W.;
RT "Cryptococcus neoformans serotype D sequencing.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
-i- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
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CC
EMBL, AA0501000004, EAL23117.1, -, Genomic_DNA.
DR GO:0005875; C:microtubule associated complex; IEA.
DR GO:0005524; F:ATP binding; IEA.
DR GO:0003777; F:microtubule motor activity; IEA.

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Query Match	48.0%	Score 1932.5	DB 2	Length 1556	
Beat local similarity	53.0%	Pred. No. 8.4e-90			
Matches	420	Conservative 99	Mismatches 190	Indels 83	Gaps 14
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Dr	InterPro; IPR001849; PH.				
Dr	InterPro; IPR01993; PH_type.				
Dr	Pfam; PF00498; FHA; 1.				
Dr	Pfam; PF00225; kinesin; 1.				
Dr	Pfam; PF00169; PH; 1.				
Dr	PRINTS; PR00380; KINESINHEAVY.				
Dr	SMART; SM00129; Kisc; 1.				
Dr	SMART; SM00233; PH; 1.				
Dr	PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.				
Dr	PROSITE; PS00667; KINESIN MOTOR DOMAIN2; 1.				
Dr	PROSITE; PS00003; PH_DOMAIN; 1.				
KM	Hypothetical protein.				
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Beat local similarity	53.0%	Pred. No. 8.4e-90			
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Dr	GO: 0007018; P: microtubule-based movement; IEA.				
Dr	InterPro; IPR001752; kinesin_motor.				
Dr	InterPro; IPR001849; PH.				
Dr	InterPro; IPR01993; PH_type.				
Dr	Pfam; PF00498; FHA; 1.				
Dr	Pfam; PF00225; kinesin; 1.				
Dr	Pfam; PF00169; PH; 1.				
Dr	PRINTS; PR00380; KINESINHEAVY.				
Dr	SMART; SM00129; Kisc; 1.				
Dr	SMART; SM00233; PH; 1.				
Dr	PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.				
Dr	PROSITE; PS00667; KINESIN MOTOR DOMAIN2; 1.				
Dr	PROSITE; PS00003; PH_DOMAIN; 1.				
KM	Hypothetical protein.				
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Query Match	48.0%	Score 1932.5	DB 2	Length 1556	
Beat local similarity	53.0%	Pred. No. 8.4e-90			
Matches	420	Conservative 99	Mismatches 190	Indels 83	Gaps 14
Dr	GO: 0007018; P: microtubule-based movement; IEA.				
Dr	InterPro; IPR001752; kinesin_motor.				
Dr	InterPro; IPR001849; PH.				
Dr	InterPro; IPR01993; PH_type.				
Dr	Pfam; PF00498; FHA; 1.				
Dr	Pfam; PF00225; kinesin; 1.				
Dr	Pfam; PF00169; PH; 1.				
Dr	PRINTS; PR00380; KINESINHEAVY.				
Dr	SMART; SM00129; Kisc; 1.				
Dr	SMART; SM00233; PH; 1.				
Dr	PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.				
Dr	PROSITE; PS00667; KINESIN MOTOR DOMAIN2; 1.				
Dr	PROSITE; PS00003; PH_DOMAIN; 1.				
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SC	SEQUENCE 1556 AA; 174143 MW; A91B635B61330354 CRC64;				
Query Match	48.0%	Score 1932.5	DB 2	Length 1556	
Beat local similarity	53.0%	Pred. No. 8.4e-90			
Matches	420	Conservative 99	Mismatches 190	Indels 83	Gaps 14
Dr	GO: 0007018; P: microtubule-based movement; IEA.				
Dr	InterPro; IPR001752; kinesin_motor.				
Dr	InterPro; IPR001849; PH.				
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Dr	Pfam; PF00225; kinesin; 1.				
Dr	Pfam; PF00169; PH; 1.				
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Dr	SMART; SM00129; Kisc; 1.				
Dr	SMART; SM00233; PH; 1.				
Dr	PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.				
Dr	PROSITE; PS00667; KINESIN MOTOR DOMAIN2; 1.				
Dr	PROSITE; PS00003; PH_DOMAIN; 1.				
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SC	SEQUENCE 1556 AA; 174143 MW; A91B635B61330354 CRC64;				
Query Match	48.0%	Score 1932.5	DB 2	Length 1556	
Beat local similarity	53.0%	Pred. No. 8.4e-90			
Matches	420	Conservative 99	Mismatches 190	Indels 83	Gaps 14
Dr	GO: 0007018; P: microtubule-based movement; IEA.				
Dr	InterPro; IPR001752; kinesin_motor.				
Dr	InterPro; IPR001849; PH.				
Dr	InterPro; IPR01993; PH_type.				
Dr	Pfam; PF00498; FHA; 1.				
Dr	Pfam; PF00225; kinesin; 1.				
Dr	Pfam; PF00169; PH; 1.				

Db 715 SETSAEQALHTS 726

RESULT 13  
OSKNG1\_CRYNE PRELIMINARY; PRT; 1556 AA.

AC OSKNG1\_CRYNE, integrated into UniProtKB/TrEMBL.  
DT 15-FEB-2005, sequence version 1.  
DT 07-FEB-2006, entry version 9.  
DE Kinesin, putative.  
GN OrderedLocustNames=CNA06610;  
OS Cryptococcus neoformans (Filobasidiella neoformans).  
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;  
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.  
NCBI\_TaxID=5207;

RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RP STRAIN=UEC21;  
RC PubMed=15653466; DOI=10.1126/science.1103773;  
RX Loftus B.J., Fung B., Roncaglia P., Rowley D., Amedeo P., Bruno D.,  
Vamshayevan J., Miranda M., Anderson J.J., Fraser J.A., Allen J.E.,  
Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,  
D'Souza C.A., Fox D.S., Grindberg V., Fu J., Fukushima M., Haas B.J.,  
Huang J.C., Janson G., Jones S.J.M., Koo H.L., Krzyzanski M.I.,  
Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Makela R.E.,  
Mathewson C.A., Mitchell T.G., Petrea M., Riggs F.R., Salzberg S.L.,  
Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,  
Suh B.B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,  
Wye N.H., Kronsted J.W., Lodge J.K., Heitman J., Davis R.W.,  
Fraser C.M., Hyman R.M.;  
RA "The genome of the basidiomycetous yeast and human pathogen  
RT Cryptococcus neoformans".  
RL Science 307.1321-1324(2005).

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EMBL, AE017341; AAM41182.1; -; Genomic DNA.  
DR GO:0005875; C-microtubule associated complex; IEA.  
DR GO:0005524; F-ATP binding; IEA.  
DR GO:0003777; F-microtubule motor activity; IEA.  
DR GO:0007018; F-microtubule-based movement; IEA.  
DR InterPro: IPR001752; FHA.  
DR InterPro: IPR001849; PH.  
DR InterPro: IPR011993; PH\_cyfe.  
DR Pfam: PF00498; FHA\_1.  
DR Pfam: PF00225; Kinesin\_1.  
DR PRINTS: PR00380; KINESINHEAVY.  
DR SMART: SM00129; KISC\_1.  
DR PROSITE: PS00411; KINESIN\_MOTOR\_DOMAIN1; 1.  
DR PROSITE: PS00067; KINESIN\_MOTOR\_DOMAIN2; 1.  
DR PROSITE: PS00003; PH\_DOMAIN; 1.  
KM Complete proteome.  
SQ SEQUENCE 1556 AA; 174210 MW; D4E65A002B9115B CRC64;

Query Match 47.0%; Score 1895; DB 2; Length 1556;  
Best Local Similarity 52.2%; Pred. No. 6,9e-88;  
Matches 412; Conservative 97; Mismatches 191; Indels 90; Gaps 13;

QY 4 GGNIKVAVRPPNAREIRGAKCIYRMGNQITLTPPGAEKARKSKTTMDGKAPA 63  
DB 3 GGNIKVAVRPPNAREIRGAKCIYRMGNQITLTPPGAEKARKSKTTMDGKAPA 59  
QY 64 FRSYVWF-DKXAPNPARQEDLFODLGVPLLDNAFGVGNCTFAYGQTSGSGSYMWYG 122  
DB 60 FDKSWISAGPKDDPRYASQQTLYEDGADLLDHSFEGFTCTFAFGQTSGSGSYMWYG 119  
QY 123 KKHGVIPIRQDMFRIN-ELQKDKNLCTVEVSYLEIYNEHVRDLNPNSTKGNLKVREH 181

Db 120 AEGKIPLTTSSELPFRIRIEMAGSDVNLSTVEVSYLEIYNEKVRDLNPNKGNLKVREH 179  
QY 182 PSTGPVYEDLAKIWNVSFOEINLEMGKARPTAATNNMETSRSNAVTTLLTQKMD 241  
DB 180 PSIGPYVEDLSRLVNEVYQMTLMDEGNARIVASTNNMETSRSNAVTTLLTQKMD 239  
QY 242 EETKMDTEKAKISLVDLGASERATSGATGALKEGAENRSISTLGRVIAALADSSG 301  
DB 240 PQTQMGKESKISLVDLGASERATSGATGATGTLKEGANINKSLTIGKISALAQGN 299  
QY 302 KQKKNQLVPRDSVLTWLLKDSLGNSMTAMIAISPADINFEETLSTLRVYASAKIKN 361  
DB 300 KRKEEHVPRDSVLTWLLKESLGNSKTMAMIAI-----STLRVYAAKIKT 348  
QY 362 HAVNEDPNAKMLRELKEELAQRLKQSSGGGGGAGSGGVSPPDTLEKQIVS 421  
DB 349 HAVNEDPNAKMLRELKEELRLSRVLSGLSD-----ESSYPSIPPEKQIVT 398  
QY 422 IQQPDATVKKMSKAEIVQOLNOSKLYRDLOTWEKLAETEEIHKEREALRELGISTE 481  
DB 399 YITKEGEIRKVTLELDQLEASEKLMESINLTWEKLOKTAIHIREKALRELGISTD 458  
QY 482 KGFVGPYHSKEMPHLVNLSDDPLAECLVYNIKPGQTRVGNVQDTQARIRLNGSKILKE 541  
DB 459 TNNVGVHAPQNHSLVNLNEDPLMSECLYQIKPGTTIAGAVDED-KAHIKLSTGHILE 517  
QY 542 HCFEENVADVNTIYVPEKAANVNGVRI--DKPTRLRSGRYIILGDFHIFRNPHEPARA 599  
DB 518 HCSFTNDEVVITIEAMPDRTFNGKRVPPNSPVKLLNFGFVTLGDSHFVRFNDPAVRA 577  
QY 600 EROEGSLHSVTNSQSGSPAPGRHRTLSKSGSDADGSRSPPLPHRKGOSDMFYAR 659  
DB 578 ERKK--LRISSTDENGLTPE-----LRPSPSRSVDTLEMDTAR 618  
QY 660 REAASAILGLDQKISHLTDELDALFDDYQKAAVRGHEVNEDEDSOSSFPVRDKYMS 719  
DB 619 REVAAD-----IEKLADQDDKLYDLDLTKRTQRRRESMDIADPSSHFRSAPLS 670  
QY 720 N-----GTDNRSFLDTAITMPTGTPRSDDGDGDLFPDGKSKODASVNDVEEL-RQOQ 770  
DB 671 NPWAGPGQTATMTNSLATPV-----GPDVDAVIVDEQSE 705  
QY 771 AQMEBALKTA 780  
DB 706 TSAEQALHTS 715

RESULT 14  
Q4VXC3\_HUMAN PRELIMINARY; PRT; 1153 AA.  
AC Q4VXC3;  
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.  
DT 07-FEB-2006, entry version 5.  
DE Kinesin family member 1B.  
GN Name=KIF1B; ORFNames=RP4-736L20.1-003;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
OC Homo.  
NCBI\_TaxID=9606;  
RN NUCLEOTIDE SEQUENCE.  
RP Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
RA Dunn M.;  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
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EMBL, AL358013; CA195222.1; -; Genomic DNA.  
DR SMR; Q4VXC3; 4-347.  
DR GO:0005874; C-microtubule; IEA.

DR GO:GO:0005875; C:microtubule associated complex; IEA.  
DR GO:GO:0005524; F:ATP binding; IEA.  
DR GO:GO:0003777; F:microtubule motor activity; IEA.  
DR GO:GO:0000166; F:nucleotide binding; IEA.  
DR GO:GO:0007018; F:microtubule-based movement; IEA.  
DR InterPro:IPR000253; FHA.  
DR InterPro:IPR01752; kinesin\_motor.  
DR Pfam:PF00498; FHA; 1.  
DR Pfam:PF00225; kinesin; 1.  
DR PRINTS:PR00380; KINESINHEAVY.  
DR SMART:SM00240; FHA; 1.  
DR SMART:SM00129; KISC; 1.  
DR PROSITE:PS50006; FHA DOMAIN; 1.  
DR PROSITE:PS00411; KINESIN MOTOR DOMAIN1; 1.  
DR PROSITE:PS50067; KINESIN MOTOR DOMAIN2; 1.  
DR ATP-binding; Microtubule\_Motor protein; Nucleotide-binding.  
KW SEQUENCE 1153 AA; 130363 MW; 6F0D846CD28311 CRC64;  
SQ

Query Match 42.0%; Score 1691; DB 2; Length 1153;  
Best Local Similarity 43.6%; Pred. No. 1,2e-77;

Matches 382; Conservative 137; Mismatches 235; Indels 122; Gaps 19;

QY 4 GGNIRVVVRPFPNAREIDRGAKCIVRMEGNOTILTPPGAEBKARKSGKTIMDGPKAPA 63  
DB 3 GASVAVAVRVRFPNAREIDRGAKCIVRMEGNOTILTPPGAEBKARKSGKTIMDGPKAPA 51  
QY 64 PDRSYWSF-DKRAPIYARQEDLFDLGVPLDLMAPGYNCCI FAYGOTGSGKSYMMGQ 122  
DB 52 FDYSYWSHTSPEDPCFASQNRVYNDIGKMLLHAEFGVNCIFAGQTAGKSYMMGQ 111  
QY 123 KEH--GVIPRICQDMFRINELQDKNLCTVEVSYLEYNERVRLDLPSTKGNLKYRE 180  
DB 112 EESQNGIIPOLCEBELFEKIND--NCNEBMSYVSVMETCYCERVDLNPKNKGLRYRE 170  
QY 181 HPSTGPYVEDLAKLVVRSFOEINLMDGNKARTVAATNMNETSSRSHAVFTLLTQKWH 240  
DB 171 HPLGLPYVEDLSKLAVTSYTDIADMDAGNKARTVAATNMNETSSRSHAVFTLVFQKGG 230  
QY 241 DEETKMDTEKVAKISLYDLAGEBRATSTGATGARKLKEGELNRSLSLTLGRVLAALDMS 300  
DB 221 DNETLSTEEKSKISLYDLAGEBRADSTAKGTRLEGNINKSLTTLAKVLSALAEVSK 290  
QY 301 GKOKNQALVPYRDSVLTWLLKDSLGGNSMTAMIAISPINFEEITSLTRYADSARKYK 360  
DB 291 -KKKTDPIFYDSVLTWLLKRENLGNSKTAIVAAISPADINVDLTSLTRADRAKQIK 349  
QY 361 NHAVVNEDNAPMIRELKEELQLRSKLOSGGGGGAGSGGPGVEEYPPPTLEKQ-- 418  
DB 350 CNAVINEDNAPMIRELKEELVRLKDLRAQGLGDIIDTSMGSLT--SSPSSCSLSQVG 407  
QY 419 ---IYSIQPDAIVKMSKAEIVEQLQNOSEKLYRDLNQTWEKRLATBEIHKERALEE 475  
DB 408 LTVSVSIQ--ERIMSTPGGEAEIERLKESEKIIAELNETWEELKRTTEAIREREELAE 465  
QY 476 LGISTEK--GFVGPYKSEMPHLVNLDDPLAECIVNIKQGQTVGVNVDQTAERL 533  
DB 466 MGAVALREDSGTIGVSPKTPPHLVNLEBPLMSCECLYIITKQITRVGADARRDITL 525  
QY 534 NGSKILKEHCTFENV---DNVVTIVPNEKAAVMNVGRIDKPTRLRSGYRIILGDFHI 588  
DB 526 SGAHKEKEHCIPRSEKSNAGEVIVTLEPCERSETYVNGKRVSQPVQLFRSGNRIIMGNH 585  
QY 589 FRENPEEARAR-----QEGLSRHSVNSQ-----LGGP 619  
DB 586 FRENPEQARAREKTPSAETPSEPVDTWTFQARELLEKQIMMKOMERKLOEMELLYK 645  
QY 620 AAGRDRTLKASGADGDSRSDS----- 643  
DB 646 EKEEADLLEQORLADSDSDSKRSGSEBSMKLITSLREKLPSPKQTIYKKGCLPSS 705  
QY 644 -----PLPHFR--GKSDWIFYARREASAILGLDQKISHLTD-----DELDAFLD 686  
DB 706 GKREPIKMYQIPQRRLSKDSKMWITISDLKIQAVKEICYEVA--LNDPFRHSQETBALAI 764

QY 667 DVQKARAVRGLVEDNEDSDSSSFVRDKYWSNCTINFSLDPAITMGFRSPDD---- 742  
DB 765 VAKKELCAMYKKQDNE-RDSIRAV-ABDWDVTVGSEKIEDWATKSGSDVDLKVH 822  
QY 743 -DGDALFFGDKKSKODASNVDEBELRQQAQWEEAL 777  
DB 823 IDKLEDILQEVKKQNMKDEELKVLRNKMLKMEKVL 858

## RESULT 15

Q4R9M8 HUMAN PRELIMINARY; PRT; 1797 AA.  
ID Q4R9M8 HUMAN

AC Q4R9M8; 19-JUL-2005, integrated into UniProtKB/TrEMBL.  
DT 19-JUL-2005, sequence version 1.

DT 07-FEB-2006, entry version 6.  
DE kinesin family member 1beta isoform III.

GN Name:KIF1Bbeta;  
OS Homo sapiens (Human);

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
OC Homo.

OC NCBI\_TaxID=9606;  
RN [1]

RP NUCLEOTIDE SEQUENCE.  
RA Munirajan A.K., Ohira M., Nakagawa A.;

RT "Identification of splicing variants of KIF1Bbeta";  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

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CC Distributed under the Creative Commons Attribution-NonCommercial license

EMBL: AB088212; BA02545.1; --; mRNA.  
DR SMR; Q4R9M8; 4-353.

DR GO:GO:0005875; C:microtubule associated complex; IEA.  
DR GO:GO:0005524; F:ATP binding; IEA.

DR GO:GO:0003777; F:microtubule motor activity; IEA.  
DR GO:GO:0007018; F:microtubule-based movement; IEA.

DR InterPro:IPR000253; FHA.  
DR InterPro:IPR001752; kinesin\_motor.

DR InterPro:IPR001849; PH.  
DR Pfam:PF00498; FHA; 1.

DR Pfam:PF00225; kinesin; 1.  
DR Pfam:PF00169; PH; 1.

DR PRINTS:PR00380; KINESINHEAVY.  
DR SMART:SM00240; FHA; 1.

DR SMART:SM00129; KISC; 1.  
DR Pfam:PF00233; PH; 1.

DR PROSITE:PS50006; FHA DOMAIN; 1.  
DR PROSITE:PS00411; KINESIN MOTOR DOMAIN1; 1.

DR PROSITE:PS50067; KINESIN MOTOR DOMAIN2; 1.  
DR PROSITE:PS50003; PH DOMAIN; 1.

SQ SEQUENCE 1797 AA; 201951 MW; 370ACFSB0BD6D15 CRC64;  
Query Match 41.8%; Score 1683.5; DB 2; Length 1797;  
Best Local Similarity 46.4%; Pred. No. 5.3e-77;

Matches 355; Conservative 126; Mismatches 173; Indels 111; Gaps 15;

QY 4 GGNIRVVVRPFPNAREIDRGAKCIVRMEGNOTILTPPGAEBKARKSGKTIMDGPKAPA 63  
DB 3 GASVAVAVRVRFPNAREIDRGAKCIVRMEGNOTILTPPGAEBKARKSGKTIMDGPKAPA 51  
QY 64 PDRSYWSF-DKRAPIYARQEDLFDLGVPLDLMAPGYNCCI FAYGOTGSGKSYMMGQ 122  
DB 52 FDYSYWSHTSPEDPCFASQNRVYNDIGKMLLHAEFGVNCIFAGQTAGKSYMMGQ 111  
QY 123 KEH--GVIPRICQDMFRINELQDKNLCTVEVSYLEYNERVRLDLPSTKGNLKYRE 180  
DB 112 EESQNGIIPOLCEBELFEKIND--NCNEBMSYVSVMETCYCERVDLNPKNKGLRYRE 170  
QY 181 HPSTGPYVEDLAKLVVRSFOEINLMDGNKARTVAATNMNETSSRSHAVFTLLTQKWH 240

```

Db      171 HPLLGPYVEDLSKLAVTSYTDIADLMDAGNKARTVAATNNNETSSRSHAVFTIVTQKH 230
Qy      241 DEETKMDTEVKATISLVDLAGSERATSTGATLKEGAINRSLSTLGRVIALADM-- 298
Db      231 DNEINLSTEVKISLVDLAGSERADSTGAKTRLKGANINKSLTTLGKVISLAEVDN 290
Qy      299 ---SSGOKKNOQVPRYDSVLTWLLKDSLGNSTWMIAAISPADINFEETLSTLRVADS 355
Db      291 CTSKSKKKKKTDPITPRDSVLTWLLRENLGNSRTAMVAALSPADINVDLTSLRYADR 350
Qy      356 AKRIKHAHVVEDPNAMIRELKEELAQLSKLQSSGG-----GGGAGSG 402
Db      351 AKQIKCNAVINEGPNAKLVRELKEEVTRLKDLRAQGLGDIIDIDPLIDYSGSGSKSM 410
Qy      403 GPVEEYPTPTPEKQ-----IVSIQOPDAIVKMSKAEIVEQUNQSEKLYRDLNQTWER 457
Db      411 GSLTSS-PSSCSLSSQVGLTSVTSIQ--ERIMSTPGGEELIERLKESEKIIAELNETWEE 467
Qy      458 KLAKEEIHKEBPAALEELGISIEK--GFVGPYHSKEMPHLVNLSDDPLAECIVYNIKP 515
Db      468 KLRKTEAIRMERBLLAEMGVAIREDGTLGVFSPKKTPHLVNLSNEDPLMSECLLYIKD 527
Qy      516 GQTRGVNVNODTQAEIRLNGSKILKEHCTPENV-----DNVVTIVPNEKAAVMVNGVRID 570
Db      528 GITRVGOADARODIVLSGAHIKEHCIPRSERSNGEVITYLPCERSETVYVNGKRV 587
Qy      571 KPTRLSGVRITIGDPHIFRNHPEERARROQSILRHSVTNSQLGSPAGRHDRTLK 630
Db      588 QPVQLRSGNRIWGNHVFERNHPEQARAEREK----- 620
Qy      631 AGSDADGDSRSDPPLPHFRGKDSDFYARRRASAAILGLDQK-----ISHLTD 678
Db      621 -----TPSAETPEEPVDWTPAOKELLEK-QGIDMKQEMEKRLQEMELIYKKEK 667
Qy      679 DELDALFDD-----VQKARAVRGLVEDNEDSDSQSSFP 712
Db      668 BEADLLLEOQRLDYESKLGALQKQVETRSLAETTEEBEEBEEVP 712

```

Search completed: September 1, 2006, 14:33:39  
 Job time : 269.166 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2006, 18:01:01 ! Search time 196 Seconds  
(without alignments)  
832.787 Million cell updates/sec

Title: US-09-235-416-1\_COPY\_1\_357  
Perfect score: 1834  
Sequence: 1 MSGGNKIKVVRVPFNARE.....PADINFEETLSTLRVADSAK 357

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues  
Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 60 summaries

Database :  
1: A\_Geneseq.8:\*  
2: geneseqp1980s:\*  
3: geneseqp1990s:\*  
4: geneseqp2000s:\*  
5: geneseqp2001s:\*  
6: geneseqp2002s:\*  
7: geneseqp2003as:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1834	100.0	784	2	AAV06618
2	1152	62.8	421	4	AAW41820
3	1152	62.8	1699	8	ABM83651
4	1152	62.8	1708	8	ABM83650
5	1152	62.8	1714	8	ABM83648
6	1152	62.8	1721	8	ABM83647
7	1152	62.8	1721	8	ABM83647
8	1152	62.8	1696	8	ABM83652
9	1142	62.3	1697	8	ABM83652
10	1142	62.3	1709	8	ABM83649
11	1142	62.3	1722	8	ABM83646
12	1119	61.0	1199	8	ABM83671
13	1119	61.0	1816	3	AAH36227
14	1119	61.0	1823	5	ABM83627
15	1117	60.9	1103	3	AAV51328
16	1117	60.9	1103	4	AAE04316
17	1117	60.9	1103	6	ABG72054
18	1117	60.9	1103	7	ADG63288
19	1114	60.7	1770	6	AAE35317
20	1112.5	60.7	1805	9	ADJ95088
21	1111	60.6	365	9	ADV50414
22	1106.5	60.3	1773	4	ABM83908
23	1063	58.0	1362	5	AAU74840

24	1063	58.0	1805	5	ABP68930	Abp68930 Human pol
25	1028	56.1	1921	4	ABM62962	Abm62962 Drosophila
26	1027.5	56.0	757	4	AAU19558	AAU19558 Human dia
27	1027.5	56.0	757	5	ABP51294	Abp51294 Human MOD
28	1020.5	55.6	762	5	ABG60124	Abg60124 Human DIT
29	1016.5	55.4	1826	7	ADJ69671	Adj69671 Human hea
30	1016.5	55.4	1826	8	ADL83235	Adl83235 Human PRO
31	1012	55.2	1844	8	ADQ97522	Adq97522 Mouse can
32	1010.5	55.1	1507	8	ADQ97525	Adq97525 Human can
33	990.5	54.0	1815	8	ADP66952	Adp66952 Human pro
34	990.5	54.0	1815	8	ADP66954	Adp66954 Human pro
35	990.5	54.0	1815	8	ADP66951	Adp66951 Human pro
36	990.5	54.0	1815	8	ADP66953	Adp66953 Human pro
37	987	53.8	359	5	ABM879530	Abm879530 Human kin
38	987	53.8	359	5	ABM84482	Abm84482 Human Hsk
39	987	53.8	359	5	AAE22526	AAE22526 Human Hsk
40	987	53.8	944	7	ADM04401	Adm04401 Human pro
41	987	53.8	944	9	AECE7331	Aec7331 Human CDN
42	987	53.8	1317	9	AEED07567	Aed07567 Chromosom
43	987	53.8	1392	6	AAE32129	Aae32129 Human CYT
44	987	53.8	1392	7	ADJ94858	Adj94858 Novel NOV
45	987	53.8	1393	8	ADN00367	Adn00367 Novel hum
46	951.5	51.9	1375	5	ABM879531	Abm879531 Human kin
47	951.5	51.9	1375	5	ABM84481	Abm84481 Human Hsk
48	951.5	51.9	1375	5	AAE22525	AAE22525 Human Hsk
49	947	51.6	1394	7	ADJ94856	Adj94856 Novel NOV
50	913.5	49.8	503	3	AAE63190	AAE63190 Human sec
51	911.5	49.7	504	3	AAE63189	AAE63189 Gene 5 hu
52	873	47.6	1174	4	ABM61704	Abm61704 Human KIF
53	835	45.5	366	9	ADV50400	Adv50400 Human KIF
54	835	45.5	376	9	ADV50399	Adv50399 Human KIF
55	834	45.5	354	9	ADV50396	Adv50396 Human KIF
56	834	45.5	378	9	ADV50398	Adv50398 Human KIF
57	834	45.5	388	9	ADV50397	Adv50397 Human KIF
58	834	45.5	1648	6	ADA83756	Ada83756 Human KIA
59	834	45.5	1648	8	ADQ15092	Adq15092 Human can
60	834	45.5	1648	8	ADU06498	Adu06498 Novel bro

## ALIGNMENTS

RESULT 1	AAV06618	standard; protein; 784 AA.
ID	AAV06618	
XX		
AC	AAV06618;	
XX		
DT	26-OCT-1999	(first entry)
XX		
DE	Thermomyces lanuginosus kinesin motor protein TL-gamma.	
XX		
DE	TL-gamma; kinesin; motor protein; microtubule; unc-104; infection;	
KW	neurodegenerative disease; Alzheimer's disease; Parkinson's disease;	
KW	Huntington's disease; amyotrophic lateral sclerosis.	
OS	Thermomyces lanuginosus.	
XX		
PN	WO937659-A1.	
XX		
PD	29-JUL-1999.	
XX		
PF	22-JAN-1999.	99WO-US001355.
XX		
PR	23-JAN-1998.	98US-0072361P.
XX		
PA	(REGC ) UNIV CALIFORNIA.	
XX		
PI	Sakowicz R, Goldstein USB;	
XX		
DR	WPI; 1999-493950/41.	
DR	N-PSDB; AAX87656.	
XX		

PT New nucleic acid encoding microtubule motor protein, used for diagnosis  
PT of fungal infection and neurodegenerative disease.  
XX  
PS Claim 5; Page 70-71; 75pp; English.

CC This sequence represents *Thermomyces lanuginosus* Tl-gamma, a novel ATP-  
CC dependent, plus end-directed microtubule motor protein that is a member  
CC of the unc-104 family and kinesin superfamily. The invention provides Tl-  
CC gamma nucleic acids (see AA87656), proteins and antibodies, and methods  
CC of screening for Tl-gamma modulators potentially useful for treating  
CC hyphal fungal infections and diseases caused by mutated Tl-gamma, e.g.  
CC neurodegeneration involving anterograde axonal transport, such as  
CC Alzheimer's, Parkinson's or Huntington's diseases or amyotrophic lateral  
CC sclerosis. Detection of Tl-gamma allows differentiation between hyphal  
CC and non-hyphal fungal infections

XX Sequence 784 AA;

Query Match 100.0%; Score 1834; DB 2; Length 784;  
Best Local Similarity 100.0%; Pred. No. 5, 4e-172;  
Matches 357; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGGNIKVVVRVPFPNAREIDRGAKCIYRMEGNQTILTPPGAEEKARKSGKTIWDGPK 60  
DB 1 MSGGNIKVVVRVPFPNAREIDRGAKCIYRMEGNQTILTPPGAEEKARKSGKTIWDGPK 60  
QY 61 AAFDPSYSPDKNAPNVARQEDLPDLGVPLLDNAFKGNNCIPAYGOTSGSKSYMMG 120  
DB 61 AAFDPSYSPDKNAPNVARQEDLPDLGVPLLDNAFKGNNCIPAYGOTSGSKSYMMG 120  
QY 121 YKEHGVIPRICODMERRINELQKDKNLCTVEVSYLEIYNERVRLDLPSTKGNLKVEE 180  
DB 121 YKEHGVIPRICODMERRINELQKDKNLCTVEVSYLEIYNERVRLDLPSTKGNLKVEE 180  
QY 181 HSTGTPYVEDLAKLVRSFOEINLMDENKARTVAATNMNETSSGSHAVFTLTQKMH 240  
DB 181 HSTGTPYVEDLAKLVRSFOEINLMDENKARTVAATNMNETSSGSHAVFTLTQKMH 240  
QY 241 DEETKMDTEKVAKISLVDLAGSERATSGATGARLKEGAINEINSLTIGRVIAALDMS 300  
DB 241 DEETKMDTEKVAKISLVDLAGSERATSGATGARLKEGAINEINSLTIGRVIAALDMS 300  
QY 301 GQOKNQLVPRDSVLTWLLKDSLGNMNTAMIAISPADINFEETLSTLRVADSAK 357  
DB 301 GQOKNQLVPRDSVLTWLLKDSLGNMNTAMIAISPADINFEETLSTLRVADSAK 357

RESULT 2  
AAM41820  
ID AAM41820 standard; protein; 421 AA.  
XX  
AC AAM41820;

XX 22-OCT-2001 (first entry)  
DE Human polypeptide SEQ ID NO 6751.

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;  
XX peripheral nervous system; neuropathy; central nervous system; CNS;  
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
XX chemokine; thrombolytic; drug screening; arthritis; inflammation;  
XX leukaemia.

OS Homo sapiens.  
XX  
XX WO200153312-A1.  
XX  
XX 26-JUL-2001.  
XX  
XX 26-DEC-2000; 2000WO-US034263.  
XX  
XX 23-DEC-1999; 99US-00471275.

PR 21-JAN-2000; 2000US-00488725.  
PR 25-APR-2000; 2000US-00552317.  
PR 20-JUN-2000; 2000US-00596042.  
PR 19-UTL-2000; 2000US-00620312.  
PR 03-AUG-2000; 2000US-00653450.  
PR 14-SEP-2000; 2000US-00662191.  
PR 19-OCT-2000; 2000US-00693036.  
PR 29-NOV-2000; 2000US-00727344.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D,  
PI Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
PI Zhou P, Goodrich R, Dermanac RT;  
XX  
XX WPI, 2001-442253/47.  
DR  
DR N-PSDB; AAI60976.

PT Novel nucleic acids and polypeptides, useful for treating disorders such  
as central nervous system injuries.

PS Example 2; SEQ ID NO 6751; 10078pp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and the  
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,  
CC immunosuppressant and cyostatic activity. The polynucleotides are useful  
CC in gene therapy. A composition containing a polypeptide or polynucleotide  
CC of the invention may be used to treat diseases of the peripheral nervous  
CC system, such as peripheral nervous injuries, peripheral neuropathy and  
CC localised neuropathies and central nervous system diseases, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
CC utilisation of the activities such as: Immune system suppression,  
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukaemias and  
CC C.N.S disorders. Note: The sequence data for this patent did not form  
CC part of the printed specification

XX Sequence 421 AA;

Query Match 62.8%; Score 1152; DB 4; Length 421;  
Best Local Similarity 62.1%; Pred. No. 8, 8e-105;  
Matches 226; Conservative 58; Mismatches 56; Indels 24; Gaps 6;

QY 4 GGNIKVVVRVPFPNAREIDRGAKCIYRMEGNQTILTPPGAEEKARKSGKTIWDGPKAFA 63  
DB 9 GASVYVAVRVPFPNAREIDRGAKCIYRMEGNQTILTPPGAEEKARKSGKTIWDGPKAFA 63

QY 64 FDRSYWSPDKNAP---NYARQEDLPDLGVPLLDNAFPGYNNCIPAYGOTSGSKSYMMG 120  
DB 64 FDRSYWSPDKNAP---NYARQEDLPDLGVPLLDNAFPGYNNCIPAYGOTSGSKSYMMG 120

QY 58 FDSYWS--HTSPEDINVASQKQVTRDIGEEMLQHAFFGYNCIPAYGOTSGSKSYMMG 115  
DB 58 FDSYWS--HTSPEDINVASQKQVTRDIGEEMLQHAFFGYNCIPAYGOTSGSKSYMMG 115

QY 121 YGK--EHGVIPRICODMERRINELQKDKNLCTVEVSYLEIYNERVRLDLPSTKGNLKVE 178  
DB 121 YGK--EHGVIPRICODMERRINELQKDKNLCTVEVSYLEIYNERVRLDLPSTKGNLKVE 178

QY 116 KQKXQGGIIPQLGDDLSRIDTND--NMSYSVSVSIMEICEVRLDLPSTKGNLKVE 174  
DB 116 KQKXQGGIIPQLGDDLSRIDTND--NMSYSVSVSIMEICEVRLDLPSTKGNLKVE 174

QY 179 REHSTGTPYVEDLAKLVRSFOEINLMDENKARTVAATNMNETSSGSHAVFTLTQKMH 238  
DB 179 REHSTGTPYVEDLAKLVRSFOEINLMDENKARTVAATNMNETSSGSHAVFTLTQKMH 238

QY 175 REHPLGPVEDLSKLAVTSYNDIQLDMDSGKARTVAATNMNETSSGSHAVFTLTQKMH 234  
DB 175 REHPLGPVEDLSKLAVTSYNDIQLDMDSGKARTVAATNMNETSSGSHAVFTLTQKMH 234

QY 229 WHDETKMDTEKVAKISLVDLAGSERATSGATGARLKEGAINEINSLTIGRVIAALDMS 298  
DB 229 WHDETKMDTEKVAKISLVDLAGSERATSGATGARLKEGAINEINSLTIGRVIAALDMS 298

QY 235 RHDATNTTTEKVSXISLVDLAGSERASTGKGRLEGAINEINSLTIGRVIAALDMS 294  
DB 235 RHDATNTTTEKVSXISLVDLAGSERASTGKGRLEGAINEINSLTIGRVIAALDMS 294

QY 239 SSG-----KQKQNLVPRDSVLTWLLKDSLGNMNTAMIAISPADINFEETLSTLRV 353  
DB 239 SSG-----KQKQNLVPRDSVLTWLLKDSLGNMNTAMIAISPADINFEETLSTLRV 353

QY 295 DSGPNKKKKKKTDPPIPRDSVLTWLLNENLGNMNTAMIAISPADINFEETLSTLRV 354  
DB 295 DSGPNKKKKKKTDPPIPRDSVLTWLLNENLGNMNTAMIAISPADINFEETLSTLRV 354

QY 354 DSAK 357  
DB 354 DSAK 357

QY 355 DRAK 358  
DB 355 DRAK 358

RESULT 3  
ID ABM83651 standard; protein; 1699 AA.  
XX  
AC ABM83651;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Human diagnostic and therapeutic protein SEQ ID NO:3900.  
XX  
KM Gene therapy; human diagnostic and therapeutic polynucleotide; dithp.  
XX  
OS Homo sapiens.  
XX  
PN WO2004023973-A2.  
XX  
PD 25-MAR-2004.  
XX  
PF 12-SEP-2003; 2003WO-US028227.  
PR 12-SEP-2002; 2002US-0410259P.  
PR 12-SEP-2002; 2002US-0410260P.  
XX  
(INCY-) INCYTE CORP.  
XX  
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,  
PI Harthorne TA, Suchorolski MT, Altus CM, Plets SJ, Elder LV,  
PI Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP;  
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;  
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;  
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kitton ES,  
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D,  
PI Patury S, Shi X, Suarez CU;  
XX  
DR MPI; 2004-329368/30.  
DR N-Psdb; ACN42303.  
XX  
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful  
PT in diagnosing a condition, disease or disorder associated with human  
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
PT in gene mapping.  
XX  
XX  
XX Claim 27; Page; 190pp; English.  
XX  
CC The invention relates to novel diagnostic and therapeutic polynucleotides  
CC selected from one of the 2722 sequences defined in the specification. A  
CC polynucleotide of the invention may have a use in gene therapy. The human  
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be  
CC used to diagnose a particular condition, disease or disorder associated  
CC with human molecules, e.g. cell proliferative disorders,  
CC autoimmune/inflammatory disorder, developmental disorders, endocrine  
CC disorder, neurological disorders, gastrointestinal disorders, or  
CC infections caused by virus, bacteria, fungi or parasite. The dithp  
CC molecules may also be used in genetic mapping, in identifying individuals  
CC from minute biological samples, in detecting single nucleotide  
CC polymorphisms, as molecular weight markers, and for somatic or germline  
CC gene therapy. The present sequence data represents a dithp protein of the  
CC invention. Note: The sequence data for this patent is not represented in  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)  
XX  
XX Sequence 1699 AA;  
XX  
Query Match 62.8%; Score 1152; DB 8; Length 1699;  
Best Local Similarity 62.1%; Pred. No. 8.6e-104;  
Matches 226; Conservative 59; Mismatches 56; Indels 24; Gaps 6;  
QY 4 GGNIKVAVRPPNNAEIDRGACIVRMENQITLTPPECAEKKARKSGKTITDGPAPR 63  
DB 3 GASVRAVAVRPPNNAEIDRGACIVRMENQITLTPPECAEKKARKSGKTITDGPAPR 63  
QY 64 FRSYVSPDKNAF---NVARQEDLPDLDGVPILLDNAFKYGNNCIFAYGQTGSKSYVMWG 120

DB 52 FDYSYMS--HTSPEDINTYASQKQVARDISEBMLQHPFEGYNCIFPYGQTGAKSKITMNG 109  
QY 121 YGR--EHWIPIRICODMFRINELQDKNLCTVEVSYLIEYNERVDDLNPSTKGNLKY 178  
DB 110 KQEKDQGGIIPQCEDLFGSRINDTND--NMSYSEVSYMEYCERVDLLNPKGNLRY 168  
QY 179 REHPSTGPIYVEDLAKLVYRSFOEIENTLMBEGNKAARTVAATNNMETSSRSRAVPTLLTQK 238  
DB 169 REHPLLGPIYVEDLSKLAVTSYNDIIDLMDSGNKAARTVAATNNMETSSRSRAVPTLLTQK 228  
QY 239 WHDEETKMDTEKVAKISLVDLAGSEBRTSGATGARLKEGAEINRSISTLGRVIAALADW 298  
DB 229 RHDATNITTEKYSKISLVDLAGSEBRTSGATGARLKEGAEINRSISTLGRVIAALAEW 288  
QY 299 SSG----KQKNQVLVPYRDSVLTWLLKDSLGNSTAMI AISPADINEFTLSTLRYA 353  
DB 289 DSGPNKKNKKKKKTDFPYRDSVLTWLLRENLGNSRSTAAV AALSPADINDEFTLSTLRYA 348  
QY 354 DSAK 357  
DB 349 DRAX 352  
RESULT 4  
ID ABM83650 standard; protein; 1708 AA.  
XX  
AC ABM83650;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Human diagnostic and therapeutic protein SEQ ID NO:3899.  
XX  
KM Gene therapy; human diagnostic and therapeutic polynucleotide; dithp.  
XX  
OS Homo sapiens.  
XX  
PN WO2004023973-A2.  
XX  
PD 25-MAR-2004.  
XX  
PF 12-SEP-2003; 2003WO-US028227.  
PR 12-SEP-2002; 2002US-0410259P.  
PR 12-SEP-2002; 2002US-0410260P.  
XX  
(INCY-) INCYTE CORP.  
XX  
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,  
PI Harthorne TA, Suchorolski MT, Altus CM, Plets SJ, Elder LV,  
PI Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP;  
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;  
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;  
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kitton ES,  
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D,  
PI Patury S, Shi X, Suarez CU;  
XX  
DR MPI; 2004-329368/30.  
DR N-Psdb; ACN42302.  
XX  
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful  
PT in diagnosing a condition, disease or disorder associated with human  
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
PT in gene mapping.  
XX  
XX Claim 27; Page; 190pp; English.  
XX  
CC The invention relates to novel diagnostic and therapeutic polynucleotides  
CC selected from one of the 2722 sequences defined in the specification. A  
CC polynucleotide of the invention may have a use in gene therapy. The human  
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be  
CC used to diagnose a particular condition, disease or disorder associated

CC with human molecules, e.g. cell proliferative disorders, endocrine  
CC autoimmune/inflammatory disorder, developmental disorder, endocrine  
CC disorder, neurological disorders, gastrointestinal disorders, or  
CC infections caused by virus, bacteria, fungi or parasite. The dithp  
CC molecules may also be used in genetic mapping, in identifying individuals  
CC from minute biological samples, in detecting single nucleotide  
CC polymorphisms, as molecular weight markers, and for somatic or germline  
CC gene therapy. The present sequence represents a dithp protein of the  
CC invention. Note: The sequence data for this patent is not represented in  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)

SQ Sequence 1708 AA;

Query March	62.8%;	Score 1152;	DB 8;	Length 1708;
Best Local	62.1%;	Pred. No. 8.7e-104;		
Matches 226;	Conservative	58;	Mismatches 56;	Indels 24;
				Gaps 6;

Qy	4	GGNKVVVRV	PFNAREID	RGAKCIV	REBNGNOTIL	TPPGABE	KARKSK	KTIMDP	KFA	63
Db	3	GASVKA	VARVP	FNREMS	RDSKCI	OWSGS	TTTIVN	PNQ	PET	51
Qy	64	FDRSY	SFSD	KAP---	NYARQ	EDLFQ	DGVPL	LDNAF	KYNNCIP	120
Db	52	FDYSY	YMS--	HISPE	DIN	YASQ	KOYVR	DIGEM	LQAF	109
Qy	121	YGR-	EHGV	IPRIC	ODMFR	INEL	OKDKN	LCTVE	VSYLEI	178
Db	110	KOE	XDOO	GII	IQ	LED	FLSR	IND	TEND-	168
Qy	179	REH	ST	STPY	VED	LAK	LVRS	FQEI	ENLMD	238
Db	169	REH	PL	LG	YVE	DLS	CLAV	TSYND	IOD	228
Qy	239	WHDE	TKM	DE	TE	KVAK	IS	LV	DLAG	298
Db	229	RHDE	FN	IT	TE	KVAK	IS	LV	DLAG	288
Qy	299	SSG----	KOK	KN	OL	VPY	DSV	L	TW	353
Db	289	DSG	BN	KN	KK	KK	KT	P	I	348
Qy	354	DSAK	357							
Db	349	DRAK	352							

## RESULT 5

ID ABM83648 standard; protein; 1714 AA.

AC ABM83648;

DT 18-NOV-2004 (first entry)

DE Human diagnostic and therapeutic protein SEQ ID NO:3897.

**KW** gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

OS Homo sapiens.

PN WO2004023973-A2.

PD 25-MAR-2004.

PF 12-SEP-2003; 2003WO-US028227.

PR 12-SEP-2002; 2002US-0410259P.

XX

XX

PI Harthshone TA, Suchorolski MT, Alnus AS, Pille SJ, Elder LV;  
PI Mooney EM, Deleagane AM, Panzer IS, Banville SC, Reddy TP;  
PI Stevens KA, Blanchard JU, Panzer SS, Wang X, Au AP, Gerstein EH;  
PI Peralta CH, Anderson SB, Rionx F, Shen EJ, Wu MC, Stuve LB;  
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt DA, Kitton ES;  
PI Xu Y, Kwong M, Pollick JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D,  
PI Patury S, Shi X, Suarez CJ;

DR WPI; 2004-329368/30.  
DR N-PSDB; ACN42300.

PT New diagnostic and therapeutic polynucleotides and polypeptides, useful

PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or

XX

XX

The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germ-line gene therapy. The present sequence represents a dithp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from [www.wipo.int/pct/en/sequences/11isting.htm](http://www.wipo.int/pct/en/sequences/11isting.htm)

... Sequence 1714 AA;  
SQ

Query Match	62.8%	Score 1152;	DB 8;	Length 1714;
Best Local Similarity	62.1%	Pred. No. 8.7e-10;		
Matches 226;	Conservative 58;	Mismatches 56;	Indels 24;	Gaps 6

```
Oy      4 GGNIVKVVVRVRRPNAREIDRGAKTIVRMEGNQTLTPPGAAEEKARKSGKTIMDGPXAF 63
          |::| | | | | | | | : | | | | : | | | | | | | | | | | | | |
Db      3 GASVKAARVRPFNSRMSRDSKTIOWSGSTTTIIVNPKPKET-----PKSFS 51
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64 FDRSYWSEKNAF--NYARQEDLFQDLGVPLLDNAFKGYNNCIAFGQTGSGKSYSMMG 12

Db 52 FDYSYWS--HTSPEDINYASQKQVRRDIGEEMLQHA FEGYNVCIFAYGQTGAGKSYTMMG 109

121 YGK--EHGVI<sup>Q</sup>DMFRINEL<sup>Q</sup>DKNLTCTVEVSYLEIYNERVRDLLNPSTKGNLKV 178

Db 110 KQEKDQGGIIPQLCEDLFSRINDTND-NMSYSVEVSYMEIYCERVRDLLNPKKGNLRV 168

QY 179 REHPSTGPVEDLAKLVRSFOEIEINLMDEGNKARTVAATNMNETSSRSHAVFTLLTLTÖK 238

Db 169 REHPILGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATMNETSSRSHAVENII FTQK 228

QY 239 WHDEETKMDTEKVAKISLVLAGSERATSTGATGARLKEGAEINRSLSTLGRVIALADM 298

Db 229 RHDAETNTTEKVSISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEM 288

QY 299 SSG-----KQKNQLVPRDSVLTWLLKDSLGGNSMTAMIAISPADINFEETLSTLRYA 353

Db 289 DSGPNKKKKKTDFIPYRDSVLTWLLRENLGNSRTAMVAALSPADINYDETLSTLRYA 348

QY 354 DSAK 357

Db 349 DRAK 352

ABM83647

XX ABM83647;  
 XX  
 DT 18-NOV-2004 (first entry)  
 DE Human diagnostic and therapeutic protein SEQ ID NO:3896.  
 XX gene therapy; human diagnostic and therapeutic polynucleotide; dithp.  
 KM Homo sapiens.  
 OS  
 XX MO2004023973-A2.  
 PN  
 XX PD 25-MAR-2004.  
 PP 12-SEP-2003; 2003WO-USO28227.  
 PR 12-SEP-2002; 2002US-0410255P.  
 RX 12-SEP-2002; 2002US-0410255P.  
 XX INCYTE CORP.

(INCY-) INCYTE CORP.

P1 Schmidt JF, Wright RJ, Bruns CM, Marjanovic MM, Shen F,  
 P1 Hethorn TA, Suchorolski MR, Altus CM, Pitts SJ, Elder LV,  
 P1 Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP,  
 P1 Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH,  
 P1 Perella CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LI,  
 P1 Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kirton ES,  
 P1 Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D,  
 P1 Paury S, Shi X, Suarez CJ;

DR WPI: 2004-329368/30.  
 DR N-PDB: ACN42299.

PT New diagnostic and therapeutic polynucleotides and peptides, useful  
 PT in diagnosing a condition, disease or disorder associated with human  
 PT molecules, e.g., autoimmune or inflammatory disorders, in gene therapy or  
 PS in gene mapping.

PS Claim 27; Page; 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides  
 CC selected from one of the 272 sequences defined in the specification. A  
 CC polynucleotide of the invention may have a use in gene therapy. The human  
 CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be  
 CC used to diagnose a particular condition, disease or disorder associated  
 CC with human molecules, e.g., cell proliferative disorders,  
 CC autoimmunity/inflammatory disorders, developmental disorder, endocrine  
 CC disorder, neurological disorders, gastrointestinal disorders, or  
 CC infections caused by virus, bacteria, fungi or parasite. The dithp  
 CC molecules may also be used in genetic mapping, in identifying individuals  
 CC from minute biological samples, in detecting single nucleotide  
 CC polymorphisms, as molecular weight markers, and for somatic or germline  
 CC gene therapy. The present sequence represents a dithp protein of the  
 CC invention. Note: The sequence data for this patent is not represented in  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

D6		110 KKKKQGGIIIPQLCEDLFSPRIINDTND-NMSSYSVEVSYMEIYCRVRDLPNKNKGRLRV	168
Qy		179 RHPHSTGPRIVEDLAKLVRSFOEINLMDEGNKARTVAATMMETSSRSHAVFLLITTK	238
D6		169 REHPLLGPVEDLSKLAVTSYNDIDLDMSGNKARTVAATMMNTSSRSHAVFNIFTK	228
Qy		239 WHHEFTKMPTEKYAKISLVVDLAGSRBATSGATGARLKEGAENIRSLSTIGRYAALADM	298
D6		229 RHDAEFNITTEKVSKITSLVDLAGSRBAOSTGAKGRLEKGANIKSLTLTGKVISALAEM	268
Qy		299 SSG----KOKKNQVLPPRDVSVTWMLKDSJGNSMTMAIAISPADINEETLSTURYA	353
D6		289 DSGPNRKKKKKKTDFIPYRDSVLTWLRENLGNSRTAMVAALSPADINDETSTURYA	348
Qy		354 DSAK 357	
D6		349 DRK 352	
RESULT 7			
AAM40034	ID	AAM40034 standard; protein; 893 AA.	
XX	AC	AAM40034;	
XX	DT	22-OCT-2001 (first entry)	
XX	DE	Human polypeptide SEQ ID NO 3179.	
XX	KM	Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;	
XX	KM	peripheral nervous system; neuropathy; central nervous system; CNS;	
XX	KM	Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;	
XX	KM	amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotoxic;	
XX	KM	chemokinetic; thrombolytic; drug screening; arthritis; inflammation;	
OS	OS	leukemia.	
XX	XX	Homo sapiens.	
XX	XX	WO200153112-A1.	
XX	PD	26-JUL-2001.	
XX	PF	26-DEC-2000; 200OWO-US034263.	
XX	PR	23-DEC-1999; 99US-00471275.	
XX	PR	21-JAN-2000; 200OUS-00488725.	
XX	PR	25-APR-2000; 200OUS-0052317.	
XX	PR	20-JUN-2000; 200OUS-00598042.	
XX	PR	19-JUL-2000; 200OUS-00620312.	
XX	PR	03-AUG-2000; 200OUS-00653450.	
XX	PR	14-SEP-2000; 200OUS-00662191.	
XX	PR	19-OCT-2000; 200OUS-00693036.	
XX	PR	29-NOV-2000; 200OUS-00727344.	
XX	XX	(HYSE-) HYSEQ INC.	
XX	PI	Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D, Qi,	
XX	PI	Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao J,	
XX	PI	Zhou P, Goodrich R, Drmanac RT;	
XX	DR	WPI; 2001-442253/47.	
XX	DR	N-PDB; AAI59190.	
CC	CC	The invention relates to human nucleic acids (AAI57798-AAI61369) and the	
CC	CC	encoded polypeptides (AAM38642-AAM42213) with nootropic,	
CC	CC	immunopressant and cytostatic activity. The polynucleotides are useful	
CC	CC	in gene therapy. A composition containing a polypeptide or polynucleotide	
CC	CC	as neutral nervous system injuries.	
CC	CC	Newel nucleic acids and polypeptides, useful for treating disorders such	
CC	CC	Example 4; SEQ ID NO 3179; 10078pp; English.	



XX ABM83652;  
AC  
XX  
DT 18-NOV-2004 (first entry)  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3901.  
XX  
XX gene therapy; human diagnostic and therapeutic polynucleotide; ditnp.  
XX Homo sapiens.  
XX MO2004023973-A2.  
XX  
XX 25-MAR-2004.  
XX  
XX 12-SEP-2003; 2003WO-US028227.  
XX  
XX 12-SEP-2002; 2002US-0410259P.  
XX 12-SEP-2002; 2002US-0410260P.  
XX  
XX (INCY-) INCYTE CORP.  
XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;  
PI Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;  
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;  
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;  
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve IL;  
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kitton ES;  
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;  
PI Patry S, Shi X, Suarez CJ;  
XX  
XX MPI: 2004-329368/30.  
XX N-PsDB; ACN42304.  
XX  
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful  
PT in diagnosing a condition, disease or disorder associated with human  
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
PT in gene mapping.  
XX  
XX Claim 27; Page; 190pp; English.  
XX  
XX The invention relates to novel diagnostic and therapeutic polynucleotides  
CC selected from one of the 2722 sequences defined in the specification. A  
CC polynucleotide of the invention may have a use in gene therapy. The human  
CC diagnostic and therapeutic polynucleotides (ditnp) or polypeptides may be  
CC used to diagnose a particular condition, disease or disorder associated  
CC with human molecules, e.g. cell proliferative disorders,  
CC autoimmune/inflammatory disorder, developmental disorder, endocrine  
CC disorder, neurological disorders, gastrointestinal disorders, or  
CC infections caused by virus, bacteria, fungi or parasite. The ditnp  
CC molecules may also be used in genetic mapping, in identifying individuals  
CC from minute biological samples, in detecting single nucleotide  
CC polymorphisms, as molecular weight markers, and for somatic or germ-line  
CC gene therapy. The present sequence represents a ditnp protein of the  
CC invention. Note: The sequence data for this patent is not represented in  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm  
XX  
XX Sequence 1697 AA;  
SQ

DB 110 KOEKDQGGIIPQCEDLFSPRINDTND-NMSSVSEVSWEIYCERBDLLNPKGNKLNRY 168  
QY 179 REHPSTGPYVEDLAKUVRSFOEIENTLMEGNKARVVAATNNNETSSRSHAVTLLTOK 238  
DB 169 REHPDLGPYVEDLSKIAVTSYNDIDQDMSGNARVVAATNNNETSSRSHAVNIIFTOK 228  
QY 239 MHDEETKMPTEKVAKISLVDLGSEKATSGATGATLKEGAEINRSISTLGRVIAALADW 298  
DB 229 RHDATNITTEKVKSKISLVDLGSEKATSGATGATLKEGAEINRSISTLGRVIAALADW 288  
QY 299 ---SSGKOKKNOQVLPYRDSVLTWLTLDKDSLGNSMTAMIAISPADINFEETLSTLRVADS 355  
DB 289 XPPQNKKKKKKTPRIPYRDSVLTWLTLDKDSLGNSMTAMIAISPADINFEETLSTLRVADS 348  
QY 356 AK 357  
DB 349 AK 350  
  
RESULT 10  
ID ABM83649  
ABM83649 standard; protein; 1709 AA.  
AC  
XX  
XX  
DT 18-NOV-2004 (first entry)  
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3898.  
XX  
XX gene therapy; human diagnostic and therapeutic polynucleotide; ditnp.  
XX Homo sapiens.  
XX MO2004023973-A2.  
XX  
XX 25-MAR-2004.  
XX  
XX 12-SEP-2003; 2003WO-US028227.  
XX  
XX 12-SEP-2002; 2002US-0410259P.  
XX 12-SEP-2002; 2002US-0410260P.  
XX  
XX (INCY-) INCYTE CORP.  
XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;  
PI Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;  
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;  
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;  
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve IL;  
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kitton ES;  
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;  
PI Patry S, Shi X, Suarez CJ;  
XX  
XX MPI: 2004-329368/30.  
XX N-PsDB; ACN42301.  
XX  
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful  
PT in diagnosing a condition, disease or disorder associated with human  
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
PT in gene mapping.  
XX  
XX Claim 27; Page; 190pp; English.  
XX  
XX The invention relates to novel diagnostic and therapeutic polynucleotides  
CC selected from one of the 2722 sequences defined in the specification. A  
CC polynucleotide of the invention may have a use in gene therapy. The human  
CC diagnostic and therapeutic polynucleotides (ditnp) or polypeptides may be  
CC used to diagnose a particular condition, disease or disorder associated  
CC with human molecules, e.g. cell proliferative disorders,  
CC autoimmune/inflammatory disorder, developmental disorder, endocrine  
CC disorder, neurological disorders, gastrointestinal disorders, or  
CC infections caused by virus, bacteria, fungi or parasite. The ditnp

CC molecules may also be used in genetic mapping, in identifying individuals  
CC from minute biological samples, in detecting single nucleotide  
CC polymorphisms, as molecular weight markers, and for somatic or germline  
CC gene therapy. The present sequence represents a dithp protein of the  
CC invention. Note: The sequence data for this patent is not represented in  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)

SQ Sequence 1709 AA:

Query Match 62.3%; Score 1142; DB 8; Length 1709;

Best Local Similarity 61.9%; Pred. No. 8.5e-103;

Matches 224; Conservative 59; Mismatches 57; Indels 22; Gaps 6;

```
QY 4 GGNIKVAVRPPNNAEIRGAKCIVRMEGNQITLPPPGAEEKARKSGKTIIDGPKAFA 63
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3 GASVKAIVAVRPPNSREMSRDSKCIIOMSGSTTTIVNPKPKET-----PKSFS 51
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 64 FDRSYWSPDKNAP---NYARQEDLPQDLGVPLLDNAFKGYNNCIFAYGQTSGKSYSMWG 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 52 FDIYSYWS--HTSPEDINIVASQKQVYRDIGEBMLQHAFFEGYNVCIFAYGQTGAKSKYTMWG 109
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 YGK--EHGYIPRICQDMFRRIINELQDKKULTCTVEVSYLEINERVRDLINPSTKGNLKV 178
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 110 KOEKDOQGIIPQCEDLFSRINDTND--NMSYSVEVSWEIYCERVRDLINPKNGNLKV 168
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 179 REHPSGPRVEDLAKLVRSFOEINLMDGSKARVAATNNMETSRSRSHAVFTLLTQK 238
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 169 RHPPLGPRVEDLSKLAATVSYNDIQDLMDSGNKARTVAATNNMETSRSRSHAVFNIIFTQK 228
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 239 WDEETKMDTEKVAKISLVLDAGSERATSTGATGARLKEGAEINRSLSLTGRVIALADM 298
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 229 RHDARTNITTEKYSKISLVLDAGSERADSTGAKTGLKEGANINKSLTTLGKVISALAEH 288
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 299 ---SSGKQKKNQLVPRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRVADS 355
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 289 XPPQKKKKKTDPIFYRDSVLTWLLRENLGGNSRTAMVAALSPADINDETLLSTLRVADR 348
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 356 AK 357
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 349 AK 350
```

RESULT 11

ID ABM83646 standard; protein; 1722 AA.

AC ABM83646;

DT 18-NOV-2004 (first entry)

DE Human diagnostic and therapeutic pproetin SEQ ID NO:3995.

XX gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

XX Homo sapiens.

XX WO2004023973-A2.

XX 25-MAR-2004.

XX 12-SEP-2003; 2003WO-US028227.

XX 12-SEP-2002; 2002US-0410259P.

XX 12-SEP-2002; 2002US-0410260P.

XX (INCY-) INCYTE CORP.

PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen P,  
PI Hartschorne TA, Suchorolski MT, Altus CM, Plets SJ, Elder LV,  
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP,  
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH,  
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;

PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kirton ES;  
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Glezen D;  
PI Patuary S, Shi X, Szarek CJ;  
DR WPI; 2004-329368/30.  
DR N-PEDB; ACN42298.

PT New diagnostic and therapeutic polynucleotides and polypeptides, useful  
PT in diagnosing a condition, disease or disorder associated with human  
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
PT in gene mapping.

Claim 27; Page; 190pp; English.

CC The invention relates to novel diagnostic and therapeutic polynucleotides  
CC selected from one of the 2722 sequences defined in the specification. A  
CC polynucleotide of the invention may have a use in gene therapy. The human  
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be  
CC used to diagnose a particular condition, disease or disorder associated  
CC with human molecules, e.g. cell proliferative disorders,  
CC autoimmune/inflammatory disorder, developmental disorder, endocrine  
CC disorder, neurological disorders, gastrointestinal disorders, or  
CC infections caused by virus, bacteria, fungi or parasite. The dithp  
CC molecules may also be used in genetic mapping, in identifying individuals  
CC from minute biological samples, in detecting single nucleotide  
CC polymorphisms, as molecular weight markers, and for somatic or germline  
CC gene therapy. The present sequence represents a dithp protein of the  
CC invention. Note: The sequence data for this patent is not represented in  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)

SQ Sequence 1722 AA:

Query Match 62.3%; Score 1142; DB 8; Length 1722;

Best Local Similarity 61.9%; Pred. No. 8.6e-103;

Matches 224; Conservative 59; Mismatches 57; Indels 22; Gaps 6;

```
QY 4 GGNIKVAVRPPNNAEIRGAKCIVRMEGNQITLPPPGAEEKARKSGKTIIDGPKAFA 63
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3 GASVKAIVAVRPPNSREMSRDSKCIIOMSGSTTTIVNPKPKET-----PKSFS 51
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 64 FDRSYWSPDKNAP---NYARQEDLPQDLGVPLLDNAFKGYNNCIFAYGQTSGKSYSMWG 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 52 FDIYSYWS--HTSPEDINIVASQKQVYRDIGEBMLQHAFFEGYNVCIFAYGQTGAKSKYTMWG 109
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 YGK--EHGYIPRICQDMFRRIINELQDKKULTCTVEVSYLEINERVRDLINPSTKGNLKV 178
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 110 KOEKDOQGIIPQCEDLFSRINDTND--NMSYSVEVSWEIYCERVRDLINPKNGNLKV 168
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 179 REHPSGPRVEDLAKLVRSFOEINLMDGSKARVAATNNMETSRSRSHAVFTLLTQK 238
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 169 RHPPLGPRVEDLSKLAATVSYNDIQDLMDSGNKARTVAATNNMETSRSRSHAVFNIIFTQK 228
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 239 WDEETKMDTEKVAKISLVLDAGSERATSTGATGARLKEGAEINRSLSLTGRVIALADM 298
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 229 RHDARTNITTEKYSKISLVLDAGSERADSTGAKTGLKEGANINKSLTTLGKVISALAEH 288
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 299 ---SSGKQKKNQLVPRDSVLTWLLKDSLGGNSMTAMIAAISPADINFEETLSTLRVADS 355
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 289 XPPQKKKKKTDPIFYRDSVLTWLLRENLGGNSRTAMVAALSPADINDETLLSTLRVADR 348
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 356 AK 357
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 349 AK 350
```

RESULT 12

ID ABM83671

AC ABM83671 standard; protein; 1199 AA.

DT 18-NOV-2004 (first entry)



XX Human diagnostic and therapeutic pprotein SEQ ID NO:13920.  
DE  
KM gene therapy; human diagnostic and therapeutic polynucleotide, ditbp.  
XX Homo sapiens.  
XX MO2004023973-A2.  
XX  
XX 25-MAR-2004.  
XX  
XX 12-SEP-2003; 2003WO-US028227.  
XX  
XX 12-SEP-2002; 2002US-0410259P.  
XX 12-SEP-2002; 2002US-0410260P.  
XX  
XX (INCY-) INCYTE CORP.  
XX  
XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;  
PI Harthorn TA, Suchorolski MT, Altus CM, Pitra SJ, Elder LV;  
PI Mooney EM, Deleogene AM, Panesar IS, Barville SC, Reddy TP;  
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;  
PI Peralta CH, Anderson SB, Rious P, Shen EJ, Wu MC, Stuve LJ;  
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt VA, Kiron ES;  
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;  
PI Patury S, Shi X, Suarez CJ;  
XX  
XX WPI; 2004-329368/30.  
XX N-PSDB; ACN42323.  
XX  
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful  
PT in diagnosing a condition, disease or disorder associated with human  
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
PT in gene mapping.  
XX  
XX Claim 27; Page; 190pp; English.  
XX  
XX The invention relates to novel diagnostic and therapeutic polynucleotides  
CC selected from one of the 2722 sequences defined in the specification. A  
CC polynucleotide of the invention may have a use in gene therapy. The human  
CC diagnostic and therapeutic polynucleotides (ditbp) or polypeptides may be  
CC used to diagnose a particular condition, disease or disorder associated  
CC with human molecules, e.g. cell proliferative disorders,  
CC autoimmune/inflammatory disorder, developmental disorder, endocrine  
CC disorder, neurological disorders, gastrointestinal disorders, or  
CC infections caused by virus, bacteria, fungi or parasite. The ditbp  
CC molecules may also be used in genetic mapping, in identifying individuals  
CC from minute biological samples, in detecting single nucleotide  
CC polymorphisms, as molecular weight markers, and for somatic or germline  
CC gene therapy. The present sequence represents a ditbp protein of the  
CC invention. Note: The sequence data for this patent is not represented in  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPD at www.wipo.int/pct/en/sequences/listing.htm  
XX  
XX Sequence 1199 AA;  
SQ  
Query Match 61.0%; Score 1119; DB 8; Length 1199;  
Best Local Similarity 60.8%; Pred. No. 9.1e-101;  
Matches 220; Conservative 59; Mismatches 63; Indels 20; Gaps 5;  
QY 4 GGNIRVVVRPFPNAREIDRGAKCIVRMEGNOTILTPPGAEEKARKSGKTINDGPKAPA 63  
DB 3 GASVKAIVAVRPFPNSRSTSKESKCIIOGQNSISINPKNPKP-----APKSF 51  
QY 64 FDRSYWSF-DKQNPYARQEDLPQDLGVPPLLDNAFKGYNNCIFAYGQSGSKSYMWG 122  
DB 52 FDSYSYSHSTPDPFCFASQRRVYNDIGKEMLHLAFEGYVNCIFAYGQSGSKSYMWG 111  
QY 123 KEN--GVIPRICQDMRRINELQKDKKLTCTVYSYIETINERYRLDNLSTGNLKVRE 180  
DB 112 EESQAGIIPOLCELEFKIND-NCNEMSYSVESYVEIICERVRDLNPKNGNLKRVRE 170  
QY 181 HPSTGVPVEDLAKLVVRSFQEIENLMDGKARTVAATNNNERSRSHAVFTLLTQKMH 240

DB 171 HPLGPEYVEDLSLTAATSYDIADMDAGKATVAATNNNERSRSHAVFTIVPQK 230  
QY 241 DEETKMDTEKVAKISLVDLAGSERATSTGATGARLKEGAEINSLTGVIYALADM-- 298  
DB 231 DNETNLSTKESKISLVDLAGSERADSTGAKGTRLEKGANINKSILTLGVISALAEVDN 290  
QY 299 ---SSGKQKQNOVVPVDSVLTWLLKDSIGGNSMTMIAISPADINFEETSLTRVADS 355  
DB 291 CTSKSKKKKKTDFIPYDSVLTWLLRENLGNSRTAMVAPSPADINVDLTSLTRYADR 350  
QY 356 AK 357  
DB 351 AK 352  
RESULT 13  
AAB36227  
ID AAB36227 standard; protein; 1816 AA.  
XX  
AC AAB36227;  
XX  
DT 19-FEB-2001 (first entry)  
XX  
DE Human kinesin-like protein HKLP SEQ ID NO: 4.  
XX  
XX Human, kinesin-like protein, HKLP; KIF1; cell division; cancer;  
KW intracellular transport; neurological disorder; infertility;  
KW diallelic marker; spontaneous abortion; neonatal chromosome disorder;  
KW aneuploidy.  
XX  
XX Homo sapiens.  
XX  
XX MO200063375-A1.  
XX  
XX 26-OCT-2000.  
XX  
XX 20-APR-2000; 2000WO-1B000562.  
XX  
XX 20-APR-1999; 99US-0130217P.  
XX  
XX (GENSET) GENSET.  
XX  
PI Bougueleret L, Dufaure-gare I, Grel P;  
XX WPI; 2000-665242/64.  
XX N-PSDB; AAC66550.  
XX  
XX An isolated or purified human kinesin-like protein (HKLP) encoding  
PT polynucleotide used to detect HKLP polynucleotides in a sample comprises  
PT a contiguous span of at least 12 nucleotides.  
XX  
XX Claim 46; Page 189-192; 199pp; English.  
XX  
XX The present invention describes the coding and protein sequences of the  
CC human kinesin-like protein HKLP. It is thought that the protein could be  
CC involved in neurological disorders, infertility, spontaneous abortion,  
CC neonatal chromosome disorders, aneuploidy and cancers. This is due to its  
CC function in the movement of microtubules. The protein shows homology to  
CC the murine KIF1A and KIF1B proteins. The sequences disclosed in the  
CC invention can be used in the isolation of similar human proteins and in  
CC vector production. In addition, the diallelic markers shown can be used  
CC in disease diagnosis and population studies  
XX  
XX Sequence 1816 AA;  
SQ  
Query Match 61.0%; Score 1119; DB 3; Length 1816;  
Best Local Similarity 60.8%; Pred. No. 1.8e-100;  
Matches 220; Conservative 59; Mismatches 63; Indels 20; Gaps 5;  
QY 4 GGNIRVVVRPFPNAREIDRGAKCIVRMEGNOTILTPPGAEEKARKSGKTINDGPKAPA 63  
DB 3 GASVKAIVAVRPFPNSRSTSKESKCIIOGQNSISINPKNPKP-----APKSF 51

Qy	64	FDRSVWSF-DKNA	PHYARGEDLFDQLGVLLDUNA	FKGVNNCTFAVGQTSGSKSYMMGYG	122
Db	52	FDYSYWSHTSPEDPCF	ASONRYNNIDIGKEMLHA	FGVNCIFPAVGQTAGSKSYTMGKQ	111
Qy	123	KEH--GVVPRICQDM	FRRIINELQDKNLTCTVE	SVSLYEIYNERVRLDLPSTGKLVRE	180
Db	112	ESQSGIITPOLCEEL	LFKIND-NCNBEMS	SVSEVSMETICEVRRLDLPKKNGNLRVE	170
Qy	181	HPSTGPPYEDLAKLV	VRSEFOEILEMDEGN	KARTVAATYNNETSSSHAVFTLTLOKKN	240
Db	171	HPLLGPYVEDLSKL	AVTSYTDIADLMDA	DNKARTVAATYNNETSSSRSHAVFTLVFOKKG	230
Qy	241	DEETKMDIEKVAKI	SLVLDAGESEARTSG	TAGTARLKEGAEINRSJLTLGRVIAALDD--	298
Db	231	DNETLSTKESKISL	VLDLAGSERADSTG	KGTRLEKANINISLTLLGKVISALAEVDN	290
Qy	299	--SSGKQKQNLV	VRDVSVLTWLLKDS	LGGNSMTAMIAAISPADINFEETLSTLRVADS	355
Db	291	CTSKSKKKKKTDF	IYRDSVLTWLLRE	NGNSRTAMVAAISPADINDETLLSTLRVADR	350
Qy	356	AK	357		
Db	351	AK	352		

RESULT 14

ABB07867	1D	ABB07867	standard; protein; 1823 AA.
XX	XX	ABB07867;	
DT	03-JUL-2002	(first entry)	
DE	Human kinesin-associated protein having motor domain.		
KM	Human; kinesin-associated protein; motor domain; cytoslatic; KIF1B-beta; neuroblastoma.		
OS	Homo sapiens.		
PN	MO200226965-A1.		
PD	04-APR-2002.		
PF	01-OCT-2001; 2001WO-JP008635.		
PR	29-SEP-2000; 2000JP-00300247.		
PA	(HISM ) HISAMITSU PHARM CO LTD.		
PA	(CHIB-) CHIBA PREFECTURE.		
PI	Nakagawara A;		
DR	WPI; 2002-340013/37.		
DR	N-PSDB; ABL40908.		
PT	Gene encoding human kinesin-associated protein with motor domain, useful for diagnosis and treatment of neuroblastoma.		
PS	Claim 2; Page 40-48; 57pp; Japanese.		

The invention provides a human kinesin-associated gene encoding a protein having a motor domain and another protein encoded by the human kinesin-associated gene having no motor domain. The genes are useful for the diagnosis and treatment of human neuroblastoma, and judgement of prognosis of this disease. Also provided are probes and primers hybridising to part of the KIF1B-beta gene, useful for diagnosing neuroblastoma in which the gene sequence is detected in tissue samples. The present sequence represents a human kinesin-associated protein having the motor domain

Sequence 1823 AA;

Query Match	61.0%;	Score 1119;	DB 5;	Length 1823;
Best Local Similarity	60.8%;	Pred. No. 1.8e-100;		
Matches 220;	Conservative	59;	Mismatches 63;	Indels 20;
			Gaps	5
QY	4	GNKIKVVVRVRFNFARREIDRGAKCIVMEGNOIILTPPEPKAEKARKSGKTIIMDGPKAFA	63	
Db	3	GA5VKVAVRVRFPFNRSETSKESKCIILQIQGNSTSIINDKNPKE-----APKFS	51	
QY	64	FDRISYNSF-DKMANVYARQEDLPDDLGVPLLDNAFKGTNNCIIFAYGQTSKSGSYMMGQ	122	
Db	52	FDYSYMSHTSEDEDCFPASQNRVYNDIGEMILHAFEGNVCIIFAYGQAGAGSYMMGQ	111	
QY	123	KEH--GVYPRICQMPFRINELQDKULTVEVSYLEIYNERVARDLNPSTKGLKYRE	180	
Db	112	EESQAGIILPQICELFEKIND-NCNEMSYSEVSEYMEIYERARDLNPKNKGLRARE	170	
QY	181	HPSTGPYVEDIACLVRSPQEIENLMDGKNKARTVAATNNNETSSRSHAVFTLLTQKWH	240	
Db	171	HPLLGPYVEDISKLAVTSYTDIADLMAGNKARFVAATNNNETSSRSHAVFTIVFTQKCH	230	
QY	241	DEETKMDTEKAKTSLVDLAGSEBATSGTARTGALKGAELNRSLSLGRVIALADW--	298	
Db	231	DNEFNLSITEKSKTSLVDLAGSEBASTGAIGTRLKGGANINKSLITLIGKIASALAEVDN	290	
QY	299	---SSGKQKQULVPYRDSVLTWLDLKSLSGNSMTAMIALISPADINEEYTLSTLRVADS	355	
Db	291	CTSKSKKKKKKTDFIPYRDSVLTWMLRENLGNSRTAAVVAALSPADINVEDTLSTLRVADR	350	
QY	356	AK 357		
Db	351	AK 352		

XX	RESULT 15
XX	AAVS1328
XX	ID AAVS1328 standard; protein; 1103 AA.
XX	AAVS1328;
XX	17-APR-2000 (first entry)
XX	Human KLIMP protein.
XX	DE
XX	KLIMP; kinesin-like motor protein; cytostatic; anticonvulsant; human;
XX	KM anti- $\Delta$ 12reiner; anti-Parkinsonian; antidiabetic; anti-ulcerative; cancer
XX	KM immunomodulatory; antiinflammatory; anti-AIDS; antineumatic; treatment;
XX	KM antiathletic; diagnosis; neurological disorder; vesicular transport.
XX	OS
XX	Homo sapiens.
XX	PN US6013454-A.
XX	PD 11-JAN-2000.
XX	PE 28-SEP-1998; 98US-00162373.
XX	PR 28-SEP-1998; 98US-00162373.
XX	PA (INCY-) INCYTE PHARM INC.
XX	PI Tang YT, Corley NC, Patterson C, Guegler KJ;
XX	DR WPI; 2000-126064/11.
XX	DR N-PSDB; AA244744.
XX	PT Nucleic acid sequences encoding a human kinesin-like motor protein
XX	PT (KLIMP) useful for the treatment of diseases associated with
XX	PT inappropriate KLIMP expression such as cancers, neurological disorders
XX	PT and disorders of vesicular transport.
XX	PS Claim 1; Fig 1A-J; 38pp; English.

CC This invention describes a novel human kinesin-like motor protein (KLIMP)  
CC (1) which has cytoskeletal, anticonvulsant, anti-Alzheimer's, anti-  
CC Parkinsonian, antidiabetic, anti-ulcerative, immunomodulatory,  
CC antiinflammatory, anti-AIDS, antirheumatic and antiarthritic activity.  
CC (1) and the protein it encodes may be used in the prevention, treatment  
CC and diagnosis of diseases associated with inappropriate KLIMP expression  
CC such as cancers, neurological disorders and disorders of vesicular  
CC transport. For example, (1) (and vectors containing (1) (iv)) and the  
CC KLIMP polypeptide may be used to treat disorders associated with  
CC decreased KLIMP expression such as cancers (e.g. lymphoma, melanoma and  
CC cancers of the breast lung and prostate), neurological disorders (e.g.  
CC epilepsy, Alzheimer's disease and Parkinson's disease), disorders of  
CC vesicular transport (e.g. diabetes mellitus/insipidus, Grave's disease  
CC and gastric/duodenal ulcers), and some immune/inflammatory diseases (e.g.  
CC acquired immune deficiency syndrome AIDS), rheumatoid arthritis and toxic  
CC shock syndrome). This sequence represents the human KLIMP protein  
CC described in the method of the invention  
XX  
SQ Sequence 1103 AA;  
  
Query Match 60.9%; Score 1117; DB 3; Length 1103;  
Best Local Similarity 61.6%; Pred. No. 1.3e-100;  
Matches 220; Conservative 59; Mismatches 62; Indels 16; Gaps 5;  
  
QY 4 GGNIKVAVRPFPNAREIDRGAKCIVRMEGNQITLPPGAERKARKSGKTIIDGKAPA 63  
DB 3 GASVKVAVRPFPNARETSQDAKCVSMQGNNTSINP-----KQSDAKRKSFT 51  
  
QY 64 FDRSYWSPFKNA-PNYARQEDLFQDLGVPLLDNAFGYNNCFAYGQTSGKSYMMGYG 122  
DB 52 FDRSYWSPHSTEDPQFASQOQVYRDIGEMLLHAFEGYNNCFAYGQTAGKSYTMMGRQ 111  
  
QY 123 K--EHGVIPRICODMFRINELQKKNLCTVEVSYLEIYNERVRLNPSTGKLVRE 180  
DB 112 EPGQGGIVPOLCEDLFSRVSENG-SAQLSYSVEVSWEIYCEVRDLNPKSGSLRVE 170  
QY 181 HPSGTGYVEDLAKLVVRSFOEINLMDGKARTVAATNMNNTSSSHAVFTLTLTKQKH 240  
DB 171 HPLIGYVODLSKLAVTSYADLADLMDCGNKARTVAATNMNNTSSSHAVFTLTLTKQKH 230  
  
QY 241 DEETKMDTEKVAKISIVDLAGESEATSGATGARLKEGAENRSLTGLGVIAALADMS 300  
DB 231 DQITGIDSEKVKISIVDLAGESEADSSGARGMGLKEGANINKSLTLTKGVISALADMS 290  
  
QY 301 GKQKKNQVLPYRDSVLTWLLKDSLGNNSMTAMIAISPADINEFTLSTLRVADSAK 357  
DB 291 -KKRKSDFIPYRDSVLTWLLKENLGNSTRMTAMIAALSPADINEFTLSTLRVADRTK 346  
  
RESULT 16  
AAE04316  
ID AAE04316 standard; protein; 1103 AA.  
XX  
AC AAE04316;  
XX  
DT 10-SEP-2001 (first entry)  
XX  
DE Human kinesin-like motor protein (KLIMP).  
XX  
XX Human; kinesin-like motor protein; KLIMP; cancer; adenocarcinoma;  
KW leukaemia; lymphoma; melanoma; neurological disorder; epilepsy;  
KW ischaemic cerebrovascular disease; stroke; Alzheimer's disease;  
KW Pick's disease; Huntington's disease; dementia; Parkinson's disease;  
KW vesicular transport disorder; cystic fibrosis; diabetes mellitus; AIDS;  
XX Acquired Immune Deficiency Syndrome; microbial infection.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Domain 11..377  
FT /label= Kinesin motor domain  
FT /note="This region is specifically referred in claim 1"  
FT Binding-site 97..104

FT /note="ATP-binding site"  
FT Region 242..253  
FT /note="Kinesin motor domain signature"  
XX US6248594-B1.  
XX 19-JUN-2001.  
XX 21-DEC-1999; 99US-00467946.  
XX 28-SEP-1998; 98US-00162373.  
XX (INCY-) INCYTE GENOMICS INC.  
XX Tang YT, Corley NC, Guejler KJ, Patterson C;  
XX MPI; 2001-407322/43.  
XX N-PSDB; AAD08139.  
XX  
XX Nucleic acid sequences encoding a human kinesin-like motor protein  
XX (KLIMP) useful for the prevention and treatment of diseases associated  
XX PT with inappropriate KLIMP expression such as cancers and neurological  
XX disorders.  
XX  
XX Claim 1; Fig 1; 37pp; English.  
XX  
XX The present sequence is human kinesin-like motor protein (KLIMP) from  
XX CC Incyte clone 1281811. KLIMP and the corresponding polynucleotide are  
XX CC useful for diagnosis, treatment and prevention of disorders associated  
XX CC with decreased expression of KLIMP e.g. cancers (such as adenocarcinoma,  
XX CC leukaemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in  
XX CC particular, cancers of the adrenal gland), neurological disorders (such  
XX CC as epilepsy, ischaemic cerebrovascular disease, stroke, cerebral  
XX CC neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease,  
XX CC dementia, Parkinson's disease, peripheral nervous system disorders,  
XX CC mental disorders), and disorders of vesicular transport (such as cystic  
XX CC fibrosis, diabetes mellitus, AIDS (Acquired Immune Deficiency Syndrome),  
XX CC viral, bacterial, fungal, helminthic, and protozoal infections)  
XX  
SQ Sequence 1103 AA;  
  
Query Match 60.9%; Score 1117; DB 4; Length 1103;  
Best Local Similarity 61.6%; Pred. No. 1.3e-100;  
Matches 220; Conservative 59; Mismatches 62; Indels 16; Gaps 5;  
  
QY 4 GGNIKVAVRPFPNAREIDRGAKCIVRMEGNQITLPPGAERKARKSGKTIIDGKAPA 63  
DB 3 GASVKVAVRPFPNARETSQDAKCVSMQGNNTSINP-----KQSDAKRKSFT 51  
  
QY 64 FDRSYWSPFKNA-PNYARQEDLFQDLGVPLLDNAFGYNNCFAYGQTSGKSYMMGYG 122  
DB 52 FDRSYWSPHSTEDPQFASQOQVYRDIGEMLLHAFEGYNNCFAYGQTAGKSYTMMGRQ 111  
  
QY 123 K--EHGVIPRICODMFRINELQKKNLCTVEVSYLEIYNERVRLNPSTGKLVRE 180  
DB 112 EPGQGGIVPOLCEDLFSRVSENG-SAQLSYSVEVSWEIYCEVRDLNPKSGSLRVE 170  
QY 181 HPSGTGYVEDLAKLVVRSFOEINLMDGKARTVAATNMNNTSSSHAVFTLTLTKQKH 240  
DB 171 HPLIGYVODLSKLAVTSYADLADLMDCGNKARTVAATNMNNTSSSHAVFTLTLTKQKH 230  
  
QY 241 DEETKMDTEKVAKISIVDLAGESEATSGATGARLKEGAENRSLTGLGVIAALADMS 300  
DB 231 DQITGIDSEKVKISIVDLAGESEADSSGARGMGLKEGANINKSLTLTKGVISALADMS 290  
  
QY 301 GKQKKNQVLPYRDSVLTWLLKDSLGNNSMTAMIAISPADINEFTLSTLRVADSAK 357  
DB 291 -KKRKSDFIPYRDSVLTWLLKENLGNSTRMTAMIAALSPADINEFTLSTLRVADRTK 346  
  
RESULT 17  
ABG72054  
ID ABG72054 standard; protein; 1103 AA.

ABG72054;  
31-JAN-2003 (first entry)  
Human kinesin-like motor protein, KLIMP.  
Human; kinesin-like motor protein; KLIMP; kinesin; microtubule motor protein; ATPase; force; directional movement; agonist; antagonist; diagnostic; transgenic; gene therapy; cancer; neurological disorder; Alzheimer's disease; Parkinson's disease; dementia; epilepsy; vesicular transport; cystic fibrosis; hypercholesterolemia; diabetes mellitus; hyperglycaemia; hypoglycaemia; gastrointestinal disorder; ulcerative colitis; acquired immunodeficiency syndrome; AIDS; allergy; multiple sclerosis; rheumatoid arthritis; infection; human immunodeficiency virus.  
Homo sapiens.  
US2002127668-A1.  
12-SEP-2002.  
02-MAY-2001; 2001US-00847874.  
28-SEP-1998; 98US-00162373.  
21-DEC-1999; 99US-00467946.  
(INCY-) INCYTE PHARM INC.  
Tang YT, Corley NC, Guejler KJ, Patterson C; WPI; 2003-066902/06.  
N-PSDB; ABS57217.  
Novel human kinesin-like motor protein, useful in diagnosis, prevention and treatment of cancer, neurological disorders, and disorders associated with vesicular transport.  
Claim 1; Fig 1; 41pp; English.  
The invention discloses an isolated human kinesin-like motor protein (KLIMP), and the polynucleotide encoding it. Kinesins are microtubule motor proteins which have an activity that includes microtubule stimulated ATPase activity which generates force and directional movement. The KLIMP protein is useful for screening a compound for effectiveness as an agonist or antagonist, for screening a compound that specifically binds KLIMP or modulates its activity and for preparing a polyclonal or monoclonal antibody by hybridoma technology. The polynucleotide, polypeptide, antibody and compounds are useful for screening a compound for effectiveness in altering expression of a KLIMP, for assessing toxicity of a test compound, in a diagnostic test for a condition or a disease associated with the expression of KLIMP, for detecting KLIMP in a sample and for purifying KLIMP. They are also useful for creating knockin humanised animals or transgenic animals to model human diseases and in somatic or germine gene therapy. The diseases or conditions associated with a modulated expression of functional KLIMP are cancer, a neurological disorder (e.g. Alzheimer's disease, Parkinson's disease, dementia, depression, epilepsy and stroke), a disorder of the vesicular transport (e.g. cystic fibrosis, hypercholesterolaemia, diabetes mellitus, hyper- and hypoglycaemia, Grave's disease, goiter, gastrointestinal disorders such as ulcerative colitis, other conditions associated with abnormal vesicle trafficking such as acquired immunodeficiency syndrome (AIDS), allergic reactions, multiple sclerosis, rheumatoid arthritis and viral, bacterial, fungal, helminthic and protozoal infections). The sequence presented is the human KLIMP protein

QY	4	GGNKKVVRVVRPPNARELDRGAKCLYRMEGNOTILTPPGAEBKARKSGKTTIMDQKARA	63
Db	3	GASVGVAVRVRPPNARETSODAKCVASMOGNTTSIINP-----KQSKDAPKSF	51
QY	64	FDRSWSFEDKNA-PNVARQEDLFODLGVPLLDNAFKGYNNCCIFAYGQTSGSGKSYMMGYG	122
Db	52	FDYSVWSTHTSEDDPQFASQGVYRDIIGEMLLHAEGVNVCIFAYGQTGAGKSYTMMGRH	111
QY	123	K-EHGVIPRICQDMFRRINELQDKNLTCTVEVSYLEYINERVDLNPSTKNAKYRE	180
Db	112	EPGQGVIPQCEDELFGRVSEHQ-SAQSYSEVSYMEYICRVADLNPMSKRGSLRVE	170
QY	181	HPSTGPEYVEDLAKLVRSFOEIEMLMDGKNKRYTAATNMNETSSRSHAVFTLTLOKH	240
Db	171	HPILGPPYQDLSKLAVTSYADLADMDGKNKRYTAATNMNETSSRSHAVFTLVFQRCH	230
QY	241	DEETKMDTEKYAKISLVDLAGSERATSGATGARLKEGAENRSLSITGKRVIAALADMS	300
Db	221	DQLTGIDSEKYSKISLVDLAGSERADSSGARGMGLKEGANIKSLTTLGKVISALADMS	290
QY	301	GKQKKNQVLVPRDSVLTWLTKDLSLGSNMTAMTALISPDINFEETLSLTRADASK	357
Db	291	-KKRKSDEIPRDSVLTWLTKENLGNSRTAMTALISPDINVEETLSLTRADRTK	346
RESULT 18			
ADG63388	ID	ADG63388 standard; protein; 1103 AA.	
XX	AC	ADG63388;	
XX	DT	11-MAR-2004 (first entry)	
XX	DE	Human kinesin-like motor protein, KLIMP.	
XX	KM	Human; kinesin-like motor protein, KLIMP; cancer; neurological disorder;	
KM	KM	Alzheimer's disease; Parkinson's disease;	
KM	KM	disorder of vesicular transport; cystic fibrosis; hypercholesterolaemia;	
KM	KM	diabetes; Grave's disease; Addison's disease; AIDS;	
KM	KM	autoimmune haemolytic anaemia; glomerulonephritis;	
KM	KM	inflammatory bowel disease; rheumatoid arthritis;	
KM	KM	systemic lupus erythematosus; infections; INCYTE 1281811.	
XX	OS	Homo sapiens.	
XX	PN	US2003207318-A1.	
XX	XX	06-NOV-2003.	
PF	09-JUN-2003;	2003US-00458162.	
XX	PR	28-SEP-1998;	98US-00162373.
PR	PR	21-DEC-1999;	99US-00467946.
PR	PR	02-MAY-2001;	2001US-00847874.
XX	PA	(INCY-) INCYTE CORP.	
XX	PI	Tang YT, Corley NC, Guejler KJ, Patterson C;	
XX	DR	WPI: 2003-901054/82.	
XX	DR	N-PSDB; ADG63389.	
XX	PT	New human kinesin-like motor protein and polynucleotides, useful for	
PT	PT	diagnosing, preventing or treating diseases or conditions associated with	
PT	PT	aberrant protein expression, e.g. cancer, neurological disorders, AIDS or	
XX	XX	diabetes.	
PS	Claim 1;	SEQ ID NO 1; 40pp; English.	
XX	XX		
CC	CC	The invention relates to a new isolated polypeptide comprising the human	
CC	CC	kinesin-like motor protein (KLIMP) appearing as ADG63388, a naturally-	
CC	CC	occurring amino acid sequence that is at least 90% identical to KLIMP or	
CC	CC	a biologically active or immunogenic fragment of KLIMP. Also included are	

QY	4	GGNKKVVRVVRPPNARELDRGAKCLYRMEGNOTILTPPGAEBKARKSGKTTIMDQKARA	63
Db	3	GASVGVAVRVRPPNARETSODAKCVASMOGNTTSIINP-----KQSKDAPKSF	51
QY	64	FDRSWSFEDKNA-PNVARQEDLFODLGVPLLDNAFKGYNNCCIFAYGQTSGSGKSYMMGYG	122
Db	52	FDYSVWSTHTSEDDPQFASQGVYRDIIGEMLLHAEGVNVCIFAYGQTGAGKSYTMMGRH	111
QY	123	K-EHGVIPRICQDMFRRINELQDKNLTCTVEVSYLEYINERVDLNPSTKNAKYRE	180
Db	112	EPGQGVIPQCEDELFGRVSEHQ-SAQSYSEVSYMEYICRVADLNPMSKRGSLRVE	170
QY	181	HPSTGPEYVEDLAKLVRSFOEIEMLMDGKNKRYTAATNMNETSSRSHAVFTLTLOKH	240
Db	171	HPILGPPYQDLSKLAVTSYADLADMDGKNKRYTAATNMNETSSRSHAVFTLVFQRCH	230
QY	241	DEETKMDTEKYAKISLVDLAGSERATSGATGARLKEGAENRSLSITGKRVIAALADMS	300
Db	221	DQLTGIDSEKYSKISLVDLAGSERADSSGARGMGLKEGANIKSLTTLGKVISALADMS	290
QY	301	GKQKKNQVLVPRDSVLTWLTKDLSLGSNMTAMTALISPDINFEETLSLTRADASK	357
Db	291	-KKRKSDEIPRDSVLTWLTKENLGNSRTAMTALISPDINVEETLSLTRADRTK	346
RESULT 18			
ADG63388	ID	ADG63388 standard; protein; 1103 AA.	
XX	AC	ADG63388;	
XX	DT	11-MAR-2004 (first entry)	
XX	DE	Human kinesin-like motor protein, KLIMP.	
XX	KM	Human; kinesin-like motor protein, KLIMP; cancer; neurological disorder;	
KM	KM	Alzheimer's disease; Parkinson's disease;	
KM	KM	disorder of vesicular transport; cystic fibrosis; hypercholesterolaemia;	
KM	KM	diabetes; Grave's disease; Addison's disease; AIDS;	
KM	KM	autoimmune haemolytic anaemia; glomerulonephritis;	
KM	KM	inflammatory bowel disease; rheumatoid arthritis;	
KM	KM	systemic lupus erythematosus; infections; INCYTE 1281811.	
XX	OS	Homo sapiens.	
XX	PN	US2003207318-A1.	
XX	XX	06-NOV-2003.	
PF	09-JUN-2003;	2003US-00458162.	
XX	PR	28-SEP-1998;	98US-00162373.
PR	PR	21-DEC-1999;	99US-00467946.
PR	PR	02-MAY-2001;	2001US-00847874.
XX	PA	(INCY-) INCYTE CORP.	
XX	PI	Tang YT, Corley NC, Guejler KJ, Patterson C;	
XX	DR	WPI: 2003-901054/82.	
XX	DR	N-PADB; ADG63389.	
XX	PT	New human kinesin-like motor protein and polynucleotides, useful for	
PT	PT	diagnosing, preventing or treating diseases or conditions associated with	
PT	PT	aberrant protein expression, e.g. cancer, neurological disorders, AIDS or	
XX	XX	diabetes.	
PS	Claim 1;	SEQ ID NO 1; 40pp; English.	
XX	XX		
CC	CC	The invention relates to a new isolated polypeptide comprising the human	
CC	CC	kinesin-like motor protein (KLIMP) appearing as ADG63388, a naturally-	
CC	CC	occurring amino acid sequence that is at least 90% identical to KLIMP or	
CC	CC	a biologically active or immunogenic fragment of KLIMP. Also included are	

CC an isolated polynucleotide (NA) encoding KLIMP (appearing as ADG63389, a  
CC recombinant polynucleotide comprising a promoter sequence operably linked  
CC to the KLIMP NA, a cell transformed with the recombinant polynucleotide,  
CC a transgenic organism comprising the recombinant polynucleotide, methods  
CC of producing or purifying KLIMP, an isolated antibody, which specifically  
CC binds to KLIMP, methods of detecting a target polynucleotide or KLIMP in  
CC a sample, compositions comprising the polypeptide, an agonist compound,  
CC an antagonist compound or an antibody, and an excipient, methods of  
CC treating diseases or conditions associated with decreased expression or  
CC overexpression of KLIMP, methods of screening for a compound that is  
CC effective as an agonist or antagonist of KLIMP (that specifically binds  
CC to KLIMP, that modulates the activity of KLIMP, or is effective in  
CC altering expression of the target polynucleotide), a method of screening  
CC for potential toxicity of a test compound, a diagnostic test for a  
CC condition or disease associated with the expression of KLIMP in a  
CC biological sample, methods of diagnosing a condition or disease  
CC associated with the expression of KLIMP in a subject, a method of  
CC generating an expression profile of a sample containing the  
CC polynucleotides and an array comprising different nucleotide molecules  
CC affixed at distinct physical locations on a solid substrate, where at  
CC least one nucleotide molecule comprises a first oligonucleotide or  
CC polynucleotide sequence specifically hybridizable with at least 30  
CC contiguous nucleotides of the target polynucleotide. The polypeptides and  
CC polynucleotides are useful in diagnosing, preventing or treating diseases  
CC or conditions associated with the decreased expression or overexpression  
CC of KLIMP, such as cancer, neurological disorders (e.g. Alzheimer's  
CC disease or Parkinson's disease), disorders of vesicular transport (e.g.  
CC cystic fibrosis, hypercholesterolemia, diabetes, Grave's disease or  
CC Addison's disease), AIDS, autoimmune haemolytic anaemia,  
CC glomerulonephritis, inflammatory bowel disease, rheumatoid arthritis,  
CC systemic lupus erythematosus, or infections (e.g. viral, bacterial,  
CC fungal, helminthic or protozoal). These are also useful in assessing the  
CC effects of exogenous compounds on the expression of nucleic acid and  
CC amino acid sequences of KLIMP. The KLIMP or its fragments are useful in  
CC screening compounds for effectiveness as agonist or antagonist of the  
CC polypeptides, or in altering the expression of the target polynucleotide  
CC and compounds that specifically bind to or modulate the activity of the  
CC polypeptide. The microarray is useful in monitoring or measuring protein-  
CC protein interactions, drug-target interactions, and gene expression  
CC profiles. The present sequence represents human KLIMP (INCYTE 1281811).

XX Sequence 1103 AA;

Query Match 60.9%; Score 1117; DB 7; Length 1103;

Best Local Similarity 61.6%; Pred. No. 1.3e-100;

Matches 220; Conservative 59; Mismatches 62; Indels 16; Gaps 5;

QY 4 GGNIKVVRVVRPNAREIDRGAKCIYRMENQITLTPPGAEKARKSGKTIIMDGPAFA 63  
DB 3 GASVKVAVRVRPNAREIDRGAKCIYRMENQITLTPPGAEKARKSGKTIIMDGPAFA 51  
64 FDRSYWSF-DKNA-PNARQEDLFODLGVPLLDNAFGYNNCFAYGQTSGSKSYMMG 122

DB 52 FDRSYWSHSTSTEDPOFASQOQVVRDIEGEMILHAFEGYNNCFAYGQTSGSKSYMMGRQ 111  
QY 123 K--EHGVIPRICODMRRINELQDKNLTCTVEVSYLEINERVRDLNPNSTGNLKYRE 180

DB 112 EPGQOQIVPOLCEDLFSRVSBNQ-SAGLSYSVEVSYLEINERVRDLNPNSTGNLKYRE 170  
QY 181 HPSTGTYVEDLAKLVRSFOEINLMDGKARVTVAATNNNETSSRSHAVFTLTTLQKMH 240

DB 171 HPLIGYVVDLSKLAATSVADIADLMDGKARVTVAATNNNETSSRSHAVFTLIVFQKCH 230  
QY 241 DEETKMDTEKVAKISLVDLAGSRATSTGATGARLKEGAINRSLSLTGAVIAALADMS 300

DB 231 DQLTGIDSEKYSISLVDLAGSRADSSGARGMKLKGAINRSLSLTGAVISALADMS 290  
QY 301 GKGKQKQVLVYRVSYSVLTWILKDSLGNSGNTAMTAASPADINFEETSLTRYDSAK 357

DB 291 -KRRKSDPIYRDSVLTWILKENLKGNSRTAMTAASPADINFEETSLTRYADRTK 346

RESULT 19

AAE35317  
ID AAE35317 standard; protein; 1770 AA.

XX AAE35317;

XX 17-JUN-2003 (first entry)

XX Mouse KIF1Bbeta protein.

XX KIF1B protein; gene therapy; molecular motor protein; kinesin; mouse;  
KW KIF1Bbeta gene-associated disease; Charcot-Marie-Tooth disease type 2A;  
XX muscular; transgenic.

OS Mus musculus.

XX W0200297079-A2.

XX 05-DEC-2002.

XX 29-MAY-2002; 2002MO-JP005226.

XX 29-MAY-2001; 2001US-0293513P.

XX (UYTY ) UNIV TOKYO.

XX Hirokawa N, Hayashi Y;

XX WPI; 2003-167270/16.

XX N-PSDB; AAD53964.

PT New KIF1Bb polypeptide having motor activity that transports synaptic  
PT vesicle precursor, is useful for developing therapeutic or preventive  
PT agent for Kif1Bb gene-associated diseases e.g. Charcot-Marie-Tooth  
PT disease type 2A.

XX Claim 1; Page 72-78; 44pp; English.

CC The invention relates to KIF1Bb protein which belongs to kinesin  
CC superfamily of molecular motor proteins (Kifs). KIF1Bb is useful for  
CC screening for a compound binding to it. Composition comprising the  
CC selected compound is useful for treating, alleviating, or preventing a  
CC Kif1Bbeta gene-associated disease, in particular Charcot-Marie-Tooth  
CC disease type 2A. Transgenic non-human vertebrate, are useful for  
CC screening for a candidate compound for treating, alleviating, or  
CC preventing a Kif1Bbeta gene-associated disease. KIF1Bb DNA is useful for  
CC gene therapy and for recombinant production of polypeptides. KIF1Bb  
CC antibody is useful for affinity purification of KIF1Bb and for detecting  
CC expression of Kif1Bbeta gene at the protein level. The present sequence  
CC is mouse KIF1Bbeta protein

XX Sequence 1770 AA;

Query Match 60.7%; Score 1114; DB 6; Length 1770;

Best Local Similarity 61.3%; Pred. No. 5.4e-100;

Matches 219; Conservative 59; Mismatches 63; Indels 16; Gaps 5;

QY 4 GGNIKVVRVVRPNAREIDRGAKCIYRMENQITLTPPGAEKARKSGKTIIMDGPAFA 63  
DB 3 GASVKVAVRVRPNAREIDRGAKCIYRMENQITLTPPGAEKARKSGKTIIMDGPAFA 51

QY 123 KEH--GVIPRICODMRRINELQDKNLTCTVEVSYLEINERVRDLNPNSTGNLKYRE 180  
DB 112 EBSQQAIIIPOLCELFKIND--NCNEMSYVSYLEINERVRDLNPNSTGNLKYRE 170

DB 52 FDRSYWSHSTSPEDPCASQNRVYNDIGKMLHAFEGYNNCFAYGQTSGSKSYMMGRQ 111  
QY 241 DEETKMDTEKVAKISLVDLAGSRATSTGATGARLKEGAINRSLSLTGAVIAALADMS 300

QY 181 HPSTGTYVEDLAKLVRSFOEINLMDGKARVTVAATNNNETSSRSHAVFTLTTLQKMH 240  
DB 171 HPLIGYVVDLSKLAATSVADIADLMDGKARVTVAATNNNETSSRSHAVFTLIVFQKCH 230

QY 241 DEETKMDTEKVAKISLVDLAGSRATSTGATGARLKEGAINRSLSLTGAVIAALADMS 300

DB 231 DETNSTKESKISLVDLAGSRADSTGKGRLEGNINNSLTTLGIVSALAEVSK 290  
QY 301 GKQKXQLVYPRDSVLTWMLKDSLGNSNTAMTAISPADINEFTLSTRYVDSK 357  
DB 291 -KKKKTDFPYRDSVLTWMLRENLGNSRTAMVAALSPADINDETLSTRYADRAK 346  
RESULT 20  
AD955088  
ID AD955088 standard; protein, 1805 AA.  
XX  
AC AD955088;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Novel NOVX protein sequence #158.  
XX  
KW antidiabetic; anorectic; cardiast; hypotensive; antiarteriosclerotic;  
KW anorectic; virucide; antibacterial; fungicide; protozoacide; nootropic;  
KW neuroprotective; antiparkinsonian; anticonvulsant; osteopathic;  
KW antidiabetic; antinflammatory; dermatological; antiaesthetic;  
KW antidiabetic; gene therapy; metabolic disorder; diabetes; obesity;  
KW infectious disease; anorexia; cancer; cardiovascular disease;  
KW hypertension; atherosclerosis; neurodegenerative disorder;  
KW Alzheimer's disease; Parkinson's disease; epilepsy; immune disorder;  
KW osteoarthritis; hematopoietic disorder; inflammatory skin disorder;  
KW asthma; dyslipidemia; neurogenesis; cell differentiation;  
KW cell proliferation; hematopoiesis; wound healing; angiogenesis;  
KW chromosome mapping; tissue typing; pharmacogenomic.  
XX  
OS Homo sapiens.  
XX  
PN WO2003040325-A2.  
XX  
PD 15-MAY-2003.  
XX  
PF 05-NOV-2002; 2002WO-US035464.  
XX  
PR 05-NOV-2001; 2001US-0338626P.  
PR 06-NOV-2001; 2001US-0333072P.  
PR 09-NOV-2001; 2001US-0348283P.  
PR 15-NOV-2001; 2001US-0335610P.  
PR 16-NOV-2001; 2001US-0338543P.  
PR 20-NOV-2001; 2001US-0331630P.  
PR 20-NOV-2001; 2001US-0331641P.  
PR 21-NOV-2001; 2001US-0332152P.  
PR 27-NOV-2001; 2001US-0333461P.  
PR 28-NOV-2001; 2001US-0333912P.  
PR 28-NOV-2001; 2001US-0334027P.  
PR 29-NOV-2001; 2001US-0334300P.  
PR 30-NOV-2001; 2001US-0334421P.  
PR 30-NOV-2001; 2001US-0334526P.  
PR 04-DEC-2001; 2001US-0336576P.  
PR 04-DEC-2001; 2001US-0336664P.  
PR 07-DEC-2001; 2001US-0338314P.  
PR 10-DEC-2001; 2001US-0338390P.  
PR 10-DEC-2001; 2001US-0339008P.  
PR 11-DEC-2001; 2001US-0339286P.  
PR 01-FEB-2002; 2002US-0353280P.  
PR 01-FEB-2002; 2002US-0353388P.  
PR 04-FEB-2002; 2002US-0354392P.  
PR 04-FEB-2002; 2002US-0354393P.  
PR 04-FEB-2002; 2002US-0354409P.  
PR 27-FEB-2002; 2002US-0359944P.  
PR 27-FEB-2002; 2002US-0360148P.  
PR 05-MAR-2002; 2002US-0361790P.  
PR 05-MAR-2002; 2002US-0361833P.  
PR 05-MAR-2002; 2002US-0361925P.  
PR 05-MAR-2002; 2002US-0362230P.  
PR 05-MAR-2002; 2002US-0362625P.  
PR 13-MAR-2002; 2002US-0364000P.

PR 13-MAR-2002; 2002US-0364181P.  
PR 13-MAR-2002; 2002US-0364182P.  
PR 13-MAR-2002; 2002US-0364197P.  
PR 13-MAR-2002; 2002US-0364227P.  
PR 17-MAY-2002; 2002US-0381621P.  
PR 17-MAY-2002; 2002US-0383675P.  
PR 28-MAY-2002; 2002US-0383675P.  
PR 17-JUL-2002; 2002US-0396703P.  
PR 06-AUG-2002; 2002US-0401552P.  
PR 07-AUG-2002; 2002US-0401594P.  
PR 07-AUG-2002; 2002US-0401787P.  
PR 15-AUG-2002; 2002US-0403619P.  
PR 20-AUG-2002; 2002US-0404821P.  
PR 23-AUG-2002; 2002US-0405368P.  
PR 23-AUG-2002; 2002US-0405402P.  
PR 23-AUG-2002; 2002US-0405496P.  
PR 23-AUG-2002; 2002US-0405631P.  
PR 26-AUG-2002; 2002US-0406125P.  
PR 04-NOV-2002; 2002US-00287226.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
PI Agee ML, Alsobrook JP, Berghs C, Boldog FL, Burgess CE, Chant JS;  
PI Chaudhuri A, DiPippo VA, Edinger SR, Eissen A, Elberman K,  
PI Gangoli EA, Gorman L, Gerlach VL, Ji W, Kekuda R, Khrantsov NV;  
PI Li L, Malvankar UM, Macdougall JR, Mezes PS, Miller CE, Millet I;  
PI Ooi CE, Ort T, Padigaru M, Patrajan M, Raselli L, Rieger DK;  
PI Rothenberg ME, Shenoy SG, Spaderna SK, Spletter KA, Taupier RJ;  
PI Vernet CM, Zernusen BD, Zhong M;  
DR WPI; 2003-441551/41.  
DR N-PSDB; AD955087.  
XX  
XX New isolated NOVX polypeptides and polynucleotides, useful for  
PT preventing, diagnosing or treating NOVX-associated disorders, e.g.  
PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,  
PT asthma, or infections.  
XX  
XX  
PS Claim 1, SEQ ID NO 316; 800pp; English.  
XX  
CC The invention relates to novel isolated polypeptides, mature forms of  
CC these, or a sequence that is at least 95 % identical to, or having one or  
CC more conservative amino acid substitutions in the polypeptides. The  
CC polypeptides, nucleic acid molecules and antibodies are useful in the  
CC manufacture of a medicament for treating a syndrome associated with a  
CC human disease, preferably a NOVX-associated disorder. The nucleic acid  
CC molecules, polypeptides and antibodies are useful for treating,  
CC preventing or diagnosing diseases such as metabolic disorders, diabetes,  
CC obesity, infectious diseases (viral, bacterial, fungal, helminthic, and  
CC protozoal), anorexia, cancer, cardiovascular diseases (hypertension,  
CC atherosclerosis), neurodegenerative disorders, Alzheimer's disease,  
CC Parkinson's disease, epilepsy, immune disorders (osteoarthritis),  
CC hematopoietic disorders, inflammatory skin disorders, asthma, and various  
CC dyslipidemias. The nucleic acids and polypeptides may also be used as  
CC targets for the identification of small molecules that modulate or  
CC inhibit e.g. neurogenesis, cell differentiation, cell proliferation,  
CC hematopoiesis, wound healing and angiogenesis, in gene therapy, in  
CC generation of antibodies that bind immunospecifically to NOVX substances  
CC for use in therapeutic or diagnostic methods. The nucleic acids are  
CC further used as hybridization probes, in chromosome mapping, tissue  
CC typing, preventive medicine, and pharmacogenomics. This sequence  
CC corresponds to one of the NOVX polypeptides of the invention.  
XX  
XX Sequence 1805 AA:  
Query Match 60.7%; Score 1112.5; DB 7; Length 1805;  
Best Local Similarity 61.5%; Pred. No. 7.9e-100;  
Matches 220; Conservative 59; Mismatches 62; Indels 17; Gaps 6;  
QY 4 GGNIKVVVRVPFNREIDRGKACIVRMENQNTILTPPGAEKARKSGKTTMDPKAPA 63  
DB 3 GASVKVAARVPFNSRETSKESKCIIMQGNSTSLINKNPE-----APKSS 51  
QY 64 FDRSYWSF-DKNAPYARQEDLFDLGVPLLDNAEKGYNNCIFAYGQSGSKSYSMMGYG 122

Db 52 FDYSYMSHTSPEDPCFASQNRVYNDIGKEMLLAHFEGYNNCFIFAYQGTGAGKSTYMWGKQ 111  
Qy 123 KEH--GVIRICODMRRIINELQDKNLTCTVEYSLEYIENVRDLINSTGNKLVRE 180  
Db 112 EESQAGIIPOLCELEPEKIND-NCNEMSYSEVSWEIYCERVRDLINPKNGNLRVRE 170  
Qy 181 HPSTGPEVDELAKLVRSFOEINLMDGKARTVAATNNNETSSRSHAVFTLTQKMH 240  
Db 171 HPLGPEVDELAKLVRSFOEINLMDGKARTVAATNNNETSSRSHAVFTLTQKMH 230  
Qy 241 DEETKMDTER-VAKISLVDLASERATSTGATGRLKEGAEINRSLSLTGRVIAALADM 299  
Db 231 DNETNSTEKVKISLVDLASERADSTGAKGRLKEGANINKSLTTLGKVISALAEVS 230  
Qy 300 SGOKKQNLVPRYDSVLTWLLKDSLGNSMTAMIAISPADINFEETLTSLRYADSAK 357  
Db 291 K-KKKKTDFIPYRDSVLTWLLRENLGNSRTAMVAALSPADINVDFTLTSLRYADRAK 347  
RESULT 21  
ADV50414 ID ADV50414 standard; protein; 365 AA.  
XX AC ADV50414;  
XX 10-MAR-2005 (first entry)  
XX DE Human KIF1B motor domain.  
XX ATPase modulator; kinesin family 1B; KIF1B; kinesin; cell proliferation;  
XX hyperproliferative disorders; cancer; breast tumor; resection;  
XX cardiovascular disease; autoimmune disease; immune disorder; arthritis;  
XX inflammation; musculoskeletal disease; graft rejection;  
XX inflammatory bowel disease; gastrointestinal disease; cytostatic;  
XX vasotropic; immunosuppressive; antiarthritic; antiinflammatory;  
XX gastrointestinal-gen.  
XX Homo sapiens.  
XX WO2004109290-A2.  
XX 16-DEC-2004.  
XX 28-MAY-2004; 2004WO-US017234.  
XX 30-MAY-2003; 2003US-0474488P.  
XX 03-JUN-2003; 2003US-0475873P.  
XX 17-MAR-2004; 2004US-0553838P.  
XX (ROSE-) ROSETTA INPHARMATICS LLC.  
XX (MERK) MERCK & CO INC.  
XX Mao M, Linaley PS, Buser CA, Marshall CG, Kim AS;  
XX WPI; 2005-057663/06.  
XX Screening for modulators of target protein e.g., kinesin family 14  
XX protein, by contacting target protein with candidate agent, and  
XX determining whether candidate agent modulates activity of target protein.  
XX Example 7; SEQ ID NO 21; 118pp; English.  
XX The invention relates to a method (M1) of screening for modulators of a  
XX target protein. The method involves contacting the target protein with  
XX candidate agent, and determining whether the candidate agent modulates  
XX activity of target protein, where the target protein comprises a sequence  
XX that has more than 80% amino acid sequence identity to a fully defined  
XX kinesin family 14 (KIF14) protein (SEQ ID No:2) or the KIF14 motor domain  
XX sequence (SEQ ID No:3). Also described are: a method (M2) for modulating  
XX cell proliferation, a method (M3) for treating a subject with a cellular  
XX hyperproliferation disorder, a method (M4) for identifying candidate  
XX subjects for treatment with an inhibitor of the activity of a target

CC protein, and a kit for screening for modulators of a target protein. A  
CC cell viability assay, cell morphology assay, cell proliferation assay,  
CC cell cycle distribution assay or apoptosis assay is used for determining  
CC whether the candidate agent modulates the activity of the target protein.  
CC The target protein comprises SEQ ID No:2, SEQ ID No:3, or a fragment of  
CC SEQ ID No:3 having Arpase activity. The modulator is an inhibitor such as  
CC RNA inhibitor, which is a KIF14 RNA inhibitor. The KIF14 RNA inhibitor  
CC comprises sequence such as those disclosed in SEQ ID Nos 8, 9 or 23.  
CC Method (M1) is useful for screening for modulators of a target protein,  
CC particularly for screening modulators of KIF14 or KIF14 motor domain.  
CC Method (M2) is useful for treating a subject with a cellular  
CC hyperproliferation disorder such as cancer, preferably breast cancer.  
CC Method (M3) is useful for treating resection, autoimmune disease,  
CC arthritis, graft rejection or inflammatory bowel disease. This sequence  
CC represents human KIF1B motor domain.  
XX SQ Sequence 365 AA;  
Query Match 60.6%; Score 1111; DB 9; Length 365;  
Best Local Similarity 60.7%; Pred. No. 8.2e-101;  
Matches 218; Conservative 59; Mismatches 62; Indels 20; Gaps 5;  
Qy 4 GGNIKVVRPFPNAREIDRGAKCIVRMEGNQITLPPGAEERKARKSGKTIINDGPKAF 63  
Db 3 GASVKVAVRPPNRSRSTESKESKCIIOGNGNSTSIINPKNPKR-----ARKSFS 51  
Qy 64 FDRSYWSF-DKQAPNARQEDLEFQDVGVPLLDAPFGYNNCFIFAYQGTGAGKSYMWGK 122  
Db 52 FDYSYMSHTSPEDPCFASQNRVYNDIGKEMLLAHFEGYNNCFIFAYQGTGAGKSTYMWGKQ 111  
Qy 123 KEH--GVIRICODMRRIINELQDKNLTCTVEYSLEYIENVRDLINSTGNKLVRE 180  
Db 112 EESQAGIIPOLCELEPEKIND-NCNEMSYSEVSWEIYCERVRDLINPKNGNLRVRE 170  
Qy 181 HPSTGPEVDELAKLVRSFOEINLMDGKARTVAATNNNETSSRSHAVFTLTQKMH 240  
Db 171 HPLGPEVDELAKLVRSFOEINLMDGKARTVAATNNNETSSRSHAVFTLTQKMH 230  
Qy 241 DEETKMDTER-VAKISLVDLASERATSTGATGRLKEGAEINRSLSLTGRVIAALADM-- 298  
Db 231 DNETNSTEKVKISLVDLASERADSTGAKGRLKEGANINKSLTTLGKVISALAEVDN 290  
Qy 299 ---SSGOKKQNLVPRYDSVLTWLLKDSLGNSMTAMIAISPADINFEETLTSLRYAD 354  
Db 291 CTSKSKKKKTDPIPYRDSVLTWLLRENLGNSRTAMVAALSPADINVDFTLTSLRYAD 349  
RESULT 22  
ABB63908 ID ABB63908 standard; protein; 1773 AA.  
XX AC ABB63908;  
XX 26-MAR-2002 (first entry)  
XX Drosophila melanogaster polypeptide SEQ ID NO 18516.  
XX Drosophila; developmental biology; cell signalling; insecticide;  
XX pharmaceutical.  
XX Drosophila melanogaster.  
XX WO200171042-A2.  
XX 27-SEP-2001.  
XX 23-MAR-2001; 2001WO-US009231.  
XX 23-MAR-2000; 2000US-0191637P.  
XX 11-JUL-2000; 2000US-00614150.  
XX (PEKE ) PE CORP NV.

PI Venter JC, Adams M, Li PWD, Myers EW;  
 XX WPI: 2001-656860/75.  
 DR N-PSDB; ABL08011.  
 XX  
 PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from *Drosophila* and for elucidating cell signaling and cell-cell  
 PT interactions.  
 XX  
 PS Disclosure; SEQ ID NO 18516; 21pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from *Drosophila*. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
 CC ABB72072). The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 1773 AA;

Query Match 60.3%; Score 1106.5; DB 4; Length 1773;  
 Best Local Similarity 62.4%; Pred. No. 3e-99;  
 Matches 222; Conservative 52; Mismatches 69; Indels 13; Gaps 4;

QY 6 NIKVVVRVPPNAREIDRGAKCIVMEGNOTILTPPGABEKARSGKTIIMGPKAFAPD 65  
 DB 32 SYKVAVRVPPNAREIDRGAKCIVMEGNOTILTPPGABEKARSGKTIIMGPKAFAPD 83  
 QY 66 RGVWFRDKKAPNVARQEDFDLQGVPLLNAPFGYNNCTFAYGQTSGSGSMWGKGE 124  
 DB 84 YGVWSHDHHDADPSTQSMWYKDI GEMLDHSPFGVNCIFAYGQTSGSGSMWGKGE 143  
 QY 125 -NGVPIRICQDMFRINELQDKNLTCTVEVSYLETYNRVRDLNPSPTGNLKVREHPS 183  
 DB 144 QGGIIPMICDLFTRIGDITBD-DLAKSYBVSIMETYCERVRDLNPKKGNIRVHEHL 202  
 QY 184 TGPVYEDLAKLVRSFOEINIMDEGNKARTVAATNMNETSSRSHAVFTLLTQKHDEE 243  
 DB 203 LCPVYEDLSKLAVTDYQDIDHLDIEGNKARTVAATNMNETSSRSHAVFTIFPQRSHDM 262  
 QY 244 TMDNPEKVAKISLVNDAGSERATSGATGARLKEGAENRSLSTGSRVIAALADMSGKQ 303  
 DB 263 TWLITTEKVKISLVNDAGSERADSTGAKGTRLEKANINKSLTTLKVISALAEVASKKK 322  
 QY 304 --KKQNLVPRDSVLTWMLKDSLGNSMTAMIAISPADINFEETLSTRYADSAR 357  
 DB 323 NTKKADFIYRDSALTWLIRENCGNSKMTAIAISPADINDETISTIRYADRAK 378

RESULT 23  
 AAU74840  
 ID AAU74840 standard; protein; 1362 AA.

AC AAU74840;

XX 10-APR-2002 (first entry)

DE Human Hskf13a protein sequence.

XX Hskf13a; human; microtubule motor protein; cytosstatic;  
 KW vulnery; antirheumatic; antiarthritic; antigout; antiinflammatory;  
 KW vasotrophic; neuroprotective; cytoskeletal; atherosclerosis; cancer;  
 KW haematopoietic tumour; tumour metastasis; benign tumour; haemangioma;  
 KW acoustic neuroma; wound healing; rheumatoid arthritis; psoriasis;  
 KW Behcet's disease; gout; gouty arthritis; angiogenesis;  
 KW rheumatoid arthritis; diabetic retinopathy; neurological disorder;  
 KW vesicular transport disorder.

OS Homo sapiens.

XX Key Location/Qualifiers  
 FH Domain 1..352  
 FT /note= "Hskf13a motor domain, this sequence is  
 FT specifically claimed in claim 8 of the specification"  
 FT Misc-difference 540  
 FT /label= Unknown  
 FT /note= "Encoded by AGN"  
 FT Misc-difference 541..563  
 FT /label= Xaa  
 FT /note= "Amino acid residues 541-563 are all Xaa, and are  
 FT all encoded by NNN"  
 FT Misc-difference 564  
 FT /label= Unknown  
 FT /note= "Encoded by NNA"  
 FT Misc-difference 747..769  
 FT /note= "Amino acid residues 747-769 are all Xaa, and are  
 FT all encoded by NNN"  
 FT Misc-difference 770  
 FT /label= Unknown  
 FT /note= "Encoded by NGR"

XX WO200192467-A2.

XX 06-DEC-2001.

XX 26-MAY-2001; 2001WO-US017148.

XX 26-MAY-2000; 2000US-00580828.

XX (CYTO-) CYTOKINETICS INC.

PI Berard C, Freedman R;

XX WPI: 2002-075464/10.

DR N-PSDB; ABR13131.

XX Human microtubule motor protein, Hskf13a, useful for screening  
 PT modulators of Hskf13a which are used for modulating cytoskeletal system  
 PT in conditions of benign tumors and rheumatoid arthritis.

XX Claim 11; Fig 2; 55pp; English.

CC This invention relates to the nucleic acid and protein sequence of a  
 CC novel microtubule motor protein Hskf13a. The protein of the invention  
 CC may have cytosstatic; vulnery; antirheumatic; antiarthritic; antigout;  
 CC antiinflammatory; vasotrophic; neuroprotective activities and may act as a  
 CC cytoskeletal system modulator. The Hskf13a nucleic acid is useful for  
 CC screening for modulators of Hskf13a, such modulators would be useful for  
 CC modulating cytoskeletal system for treating conditions such as abnormal  
 CC stimulation of endothelial cells (e.g., atherosclerosis), solid and  
 CC haematopoietic tumours and tumour metastasis, benign tumours, e.g.,  
 CC haemangiomas, acoustic neuromas, etc., abnormal wound healing, rheumatoid  
 CC arthritis, Behcet's disease, gout or gouty arthritis, diabetic  
 CC angiogenesis accompanying: rheumatoid arthritis, psoriasis, diabetic  
 CC retinopathy, etc. The sequences of the invention are useful for the  
 CC diagnosis treatment, or prevention of cancer, neurological and vesicular  
 CC transport disorders. Nucleic acids encoding the kinesins are useful for  
 CC identifying polymorphic variants, orthologues, alleles and homologues of  
 CC Hskf13a. Hskf13a and its homologues are also useful as diagnostic tools  
 CC in vitro. The kinesins and in particular their motor domains can be used  
 CC for separation of a specific ligand from a heterogeneous mixture in  
 CC aqueous solution. The kinesins and in particular their motor domains can  
 CC also be used in the field of nanotechnology. The present sequence  
 CC represents the human Hskf13a protein sequence of the invention

XX Sequence 1362 AA;

Query Match 58.0%; Score 1063; DB 5; Length 1362;  
 Best Local Similarity 60.1%; Pred. No. 4e-95;  
 Matches 212; Conservative 62; Mismatches 69; Indels 10; Gaps 5;

QY 7 IKVVVRVPPNAREIDRGAKCIVMEGNOTILTPPGABEKARSGKTIIMGPKAFAPDR 66





DR N-PSDB; ABL07065.  
XX New isolated nucleic acid detection reagent for detecting 1000 or more  
XX genes from *Drosophila* and for elucidating cell signaling and cell-cell  
PT interactions.  
XX  
XX Disclosure; SEQ ID NO 15678; 21pp + Sequence Listing; English.  
PS  
CC The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from *Drosophila*. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA  
CC sequences (AB101840-AB16175) and the encoded proteins (AB57737-  
CC AB872072). The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from Wipo.int/ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 1921 AA;

Query Match 56.1%; Score 1028; DB 4; Length 1921;  
Best Local Similarity 60.3%; Pred. No. 2.1e-91;  
Matches 213; Conservative 45; Mismatches 85; Indels 10; Gaps 4;

QY 7 IKVAVVPPFNAREIDRGAKCIVRMGNGTILTPPGAEERKARKSGKTIWDGPKAFADR 66  
Db 6 IKAVAVRPFRNREIELDTKCIEMEKQITLQNPPELEIERKQ-----PKTAFDH 58  
QY 67 STWSPFKMAPNVARQEDFDLDCVPLLDNAFKYINNCIFAYGCGSGKSYMMGYGKEHG 126  
Db 59 CFYSLNPEDENFASOETVFCVGRGLDNAFQGYNACIFAYGCGSGKSYMMGTQESKG 118  
QY 127 VPIRICQDMFRRIINELQKKNLCTVEVSLEYETINRVRPLNPS--TKGTLKREHPSGTG 185  
Db 119 IIPRLDQLESAIAN-KSTPELMYKVEVSWEIYNEVHDLPKPKNSLKVREHNVWG 177  
QY 186 PYVEDLAKLVRSFOEIEIMDEGNARFVAATNNMETSSRSRAVFTLLTQKHDEETK 245  
Db 178 PYVDGSLQALVSYQIDINLMTGKNSRTVAATNMAESSRSRAVSVLTQLTLQDQATG 237  
QY 246 MOTEKYAKISLVDLASERATSTGATGARLKGEAEINRSLSLTGRVIALADMSGKQKK 305  
Db 238 VSGEKKVSRMSLVDLASERAVKTAAGVGDRLKEGSINIKSLTTLGLVYSKLADQSNKSG 297  
QY 306 N-OLVYRPSVLTWMLKDSLGKSMTAMTAISPAINFEETLSTRYVDSAK 357  
Db 298 NDKFVYRDSVLTWMLKDNLDGNSRTVWATISPSADNTEETLSTRYADRAK 350

RESULT 26  
AAU19569  
ID AAU19569 standard; protein; 757 AA.  
XX  
AC AAU19569;  
XX  
XX 04-DEC-2001 (first entry)  
XX  
DE Human diagnostic and therapeutic polypeptide (DITHP) #155.  
XX  
XX Human; receptor; diagnostic; therapeutic; gene therapy; vaccine;  
XX cell proliferative disorder; Crohn's disease; lymphoma; leukaemia;  
XX acquired immune deficiency syndrome; AIDS; autoimmune disorder;  
XX respiratory disorder.  
OS Homo sapiens.  
XX  
XX WO200162927-A2.  
XX  
XX 30-AUG-2001.  
XX  
XX 21-FEB-2001; 2001WO-US006059.  
XX  
XX

PR 24-FEB-2000; 2000US-0184693P.  
PR 24-FEB-2000; 2000US-0184697P.  
PR 24-FEB-2000; 2000US-0184698P.  
PR 24-FEB-2000; 2000US-0184768P.  
PR 24-FEB-2000; 2000US-0184769P.  
PR 24-FEB-2000; 2000US-0184770P.  
PR 24-FEB-2000; 2000US-0184771P.  
PR 24-FEB-2000; 2000US-0184772P.  
PR 24-FEB-2000; 2000US-0184773P.  
PR 24-FEB-2000; 2000US-0184774P.  
PR 24-FEB-2000; 2000US-0184776P.  
PR 24-FEB-2000; 2000US-0184777P.  
PR 24-FEB-2000; 2000US-0184779P.  
PR 24-FEB-2000; 2000US-0184813P.  
PR 24-FEB-2000; 2000US-0184837P.  
PR 24-FEB-2000; 2000US-0184841P.  
PR 24-FEB-2000; 2000US-0185213P.  
PR 24-FEB-2000; 2000US-0185216P.  
PR 12-MAY-2000; 2000US-0203785P.  
PR 15-MAY-2000; 2000US-0204226P.  
PR 16-MAY-2000; 2000US-0204525P.  
PR 16-MAY-2000; 2000US-0204821P.  
PR 16-MAY-2000; 2000US-0204908P.  
PR 16-MAY-2000; 2000US-0205232P.  
PR 17-MAY-2000; 2000US-0204815P.  
PR 17-MAY-2000; 2000US-0204863P.  
PR 17-MAY-2000; 2000US-0205221P.  
PR 17-MAY-2000; 2000US-0205285P.  
PR 17-MAY-2000; 2000US-0205286P.  
PR 17-MAY-2000; 2000US-0205287P.  
PR 17-MAY-2000; 2000US-0205323P.  
PR 17-MAY-2000; 2000US-0205324P.  
XX  
XX (INCY- ) INCYTE GENOMICS INC.  
XX  
XX Panzer SR, Spiro PA, Benville SC, Shah P, Chalup MS, Chang SC;  
PI Chen A, D'sa SA, Amshay S, Dahl CR, Dam TC, Daniels SE, Dufour GE;  
PI Flores V, Fong WT, Greenawalt LB, Hillman JL, Jones AL, Liu TF;  
PI Roseberry AM, Rosen BH, Russo FD, Stockdreher TK, Daffo A;  
PI Wright RJ, Yap PE, Yu JY, Bradley DL, Bratcher SR, Chen W;  
PI Cohen HJ, Hodgson DM, Lincoln SE, Jackson S;  
XX  
XX MPI: 2001-502867/55.  
DR N-PSDB; AAS31140.  
XX  
XX Polynucleotides encoding diagnostic and therapeutic proteins, e.g.  
PT enzymes, hormones and receptors, useful in diagnostics and therapeutics.  
XX  
XX Claim 27; Page 488-490; 522pp; English.

XX The invention relates to polynucleotides (I) encoding diagnostic and  
CC therapeutic (DITHP) polypeptides (II), which include e.g. enzymes, and  
CC proteins involved in growth and development and receptors (I) and (II)  
CC may be used in the prevention, diagnosis and treatment of diseases  
CC associated with inappropriate DITHP expression. For example, (I) and (II)  
CC may be used to treat disorders associated with decreased polypeptide  
CC expression by rectifying mutations or deletions in a patient's genome,  
CC that affect the activity of the DITHPs, by expressing inactive proteins  
CC or supplementing the patient's own production of them (I) and (II) may  
CC be used to treat diseases, for example, cell proliferative disorder,  
CC Crohn's disease, acquired immune deficiency syndrome (AIDS), lymphoma,  
CC leukaemia, autoimmune disorders, and respiratory disorders. Additionally,  
CC (II) may be used to produce the DITHPs, by inserting the nucleic acids  
CC into a host cell and culturing the cell to express the protein. (I) and  
CC its complementary sequences may also be used as DNA probes in diagnostic  
CC assays to detect and quantitate the presence of similar nucleic acids in  
CC samples, and therefore which patients may be in need of restorative  
CC therapy. (II) may also be used as antigens in the production of  
CC antibodies against DITHPs and in assays to identify modulators of DITHP  
CC expression and activity. The anti-DITHP antibodies and antagonists may  
CC also be used to down regulate expression and activity. The anti-DITHP  
CC antibodies may also be used as diagnostic agents for detecting the  
CC presence of DITHPs in samples (e.g. by enzyme linked immunosorbant assay

CC (ELISA). AAU19415-AAU19625 represent human diagnostic and therapeutic  
CC (DITHP) polypeptides of the invention  
XX  
SQ Sequence 757 AA;  
Query Match 56.0%; Score 1027.5; DB 4; Length 757;  
Best Local Similarity 59.1%; Pred. No. 5.1e-92;  
Matches 212; Conservative 50; Mismatches 84; Indels 13; Gaps 6;  
QY 3 GGGNKKVAVRPPNAREIDRGAKCIYRMENQITLTPPGAEBKARKSKITMDGPKAF 62  
DB 17 GDSKVVAVRIRPMNRRETDLTHTKCVVDANKVILNPNTNLSKGDARGQ-----PKVF 71  
QY 63 AFDRSWSPFKNA-PNVARQEDLFQDLGVPLLDNAPFGVNNCI FAYGQTSKGSYSMMGY 121  
DB 72 AYHCHWSNDESEYKAYAGDIYFKLIGENILNAPFGVNAACIFAYGQTSKGSYSMMGT 131  
QY 122 GKEGVIPRICQDMFRINELQDKN--LTCTVEVSYLEIYNERVVDLNP-STKGNLKY 178  
DB 132 AADPGIIPRICSGLPER---TQKEENEGSPKVEVSYMEIYNEKYVDLDPKGSROTLKY 188  
QY 179 REHPSTGPIYEDLAKLVNSFOEINMDGNAKRYAATNMETSRSRAVFTLITQK 238  
DB 189 REHSVIGPYVDGLSKLAVTSYKDIESIMSEGNKSRFYAATNMEESSRSRAVFKITLTH 248  
QY 239 WHDEETKMDTEKXAKISLVNLAGSERATSGATGARLKEGAEINRSLSTIGRYTALADM 238  
DB 249 LIDVKSQTSEKQKSLVDLAGSERATKGAAGDRKESNINKSLTTLGLVISALADQ 308  
QY 299 SSGQKQKQNLVPRYDSVLTWLNDSLGNSMTAMIAISPADINFEETLSTLRVADS 357  
DB 309 SAKK-NKNKRVPRDSVLTWLNDSLGNSKTMAMVATVSPAANYDETTLTLYADRAK 366  
RESULT 27  
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KW Human; MDDT, disease detection and treatment molecule polynucleotide;  
KW proliferative disorder; hepatitis; psoriasis; cancer; AIDS;  
KW autoimmune disorder; inflammatory disorder; allergy; multiple sclerosis;  
KW rheumatoid arthritis; transgenic; gene therapy; antiretroviral;  
KW hepatotropic; anti-inflammatory; antiproliferative; cytostatic; anti-HIV;  
KW antiallergic; antianemic; antisthmatic; antithrombotic; antitumor;  
KW neuroprotective; antineumatic; antidiabetic.  
XX  
OS Homo sapiens.  
XX  
PN MO200240715-A2.  
PD 23-MAY-2002.  
PF 06-SEP-2001; 2001WO-US027628.  
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RESULT 28  
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XX  
XX Human; DITHP; diagnostic and therapeutic polypeptide; bone; testis; skin;  
KW cell proliferative disorder; cancer; tumour; autoimmune disorder; brain;  
KW inflammatory disorder; viral infection; bacterial infection; sepsis;  
KW fungal infection; parasitic infection; developmental disorder; breast;  
KW endocrine disorder; metabolic disorder; neurological disorder; cervix;  
KW gastrointestinal disorder; transport disorder; gene therapy; kidney;  
KW adrenal gland; bone marrow; lung; ovary; pancreas; prostate; spleen;  
thymus.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200220754-A2.  
PN  
XX  
XX 14-MAR-2002.  
PD  
XX 29-AUG-2001; 2001WO-US027127.  
PF  
XX 05-SEP-2000; 2000US-0229747P.  
PR 05-SEP-2000; 2000US-0229748P.  
PR 05-SEP-2000; 2000US-0229749P.  
PR 05-SEP-2000; 2000US-0229750P.  
PR 05-SEP-2000; 2000US-0229751P.  
PR 05-SEP-2000; 2000US-0230583P.  
PR 06-SEP-2000; 2000US-0230585P.  
PR 06-SEP-2000; 2000US-0230514P.  
PR 06-SEP-2000; 2000US-0230515P.  
PR 06-SEP-2000; 2000US-0230517P.  
PR 06-SEP-2000; 2000US-0230518P.  
PR 06-SEP-2000; 2000US-0230519P.  
PR 06-SEP-2000; 2000US-0230595P.  
PR 06-SEP-2000; 2000US-0230597P.  
PR 06-SEP-2000; 2000US-0230598P.  
PR 06-SEP-2000; 2000US-0230599P.  
PR 06-SEP-2000; 2000US-0230610P.  
PR 06-SEP-2000; 2000US-0230865P.  
PR 06-SEP-2000; 2000US-0230888P.  
PR 07-SEP-2000; 2000US-0230951P.  
PR 07-SEP-2000; 2000US-0231163P.  
PR 07-SEP-2000; 2000US-0231167P.  
XX  
XX (INCY-) INCYTE GENOMICS INC.  
PA  
XX Stuart J, Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman JL,  
PI Jones AL, Yu JY, Wright RO, Gietzen D, Liu TF, Yap PE, Dahl CR;

PI Momiyama MG, Bradley DL, Rohatgi SD, Harris B, Roseberry AM;  
PI Gerstein EH, Peralta CH, David MH, Panzer SR, Flores V, Daffo A;  
PI Marwaha R, Chen AJ, Chang SC, Au AP, Inman RR;  
DR WPI; 2002-383054/41.  
DR N-PSDB; ABK71715.  
XX  
XX An isolated polynucleotide useful in diagnostics and therapeutics.  
PS Claim 29; Page 637-639; 686pp; English.  
XX  
XX The invention relates to human diagnostic and therapeutic (dithp)  
CC polynucleotides and their associated polypeptides (DITHP polypeptides).  
CC The sequences of the invention are used in the treatment and diagnosis of  
CC cell proliferative disorders (e.g. atherosclerosis, cirrhosis), cancers  
CC (e.g. tumours of the adrenal gland, bone, bone marrow, brain, breast,  
CC cervix, kidney, lung, ovary, pancreas, prostate, skin, spleen, testis or  
CC thymus), autoimmune/inflammatory disorders (e.g. asthma, bronchitis,  
CC psoriasis, osteoporosis), viral infections, bacterial infections, fungal  
CC infections, parasitic infections, developmental disorders (e.g. anaemia,  
CC epilepsy), seizure disorders (e.g. cerebral palsy, spina bifida),  
CC endocrine disorders (e.g. thrombosis, aneurysm), metabolic disorders  
CC (e.g. obesity, diabetes), neurological disorders (e.g. stroke,  
CC amyotrophic lateral sclerosis, multiple sclerosis), gastrointestinal  
CC disorders (e.g. ulcerative colitis, lysinuria) and transport disorders  
CC (e.g. myotonic dystrophy, catatonias, peripheral neuropathy). Sequences  
CC ABG59943-ABG60220 represent human DITHP polypeptides of the invention  
XX  
SQ Sequence 762 AA:  
Query Match 55.6%; Score 1020.5; DB 5; Length 762;  
Best Local Similarity 58.8%; Pred. No. 2.6e-91;  
Matches 211; Conservative 50; Mismatches 85; Indels 13; Gaps 6;  
Qy 3 GGGNKKVYVRVPPFARERIDRGAQIVMEGQITLTPPEAEKARSGKTIYMPRAF 62  
Db 17 GDSKVAVARIRPMNRRETDLTHTKCVVDANKVILNPVNTLSKGDARGQ-----PKVF 71  
Qy 63 AFDRSYWSFDKNA-DNYARQEDLPFDLGVPLDANFKGNNCTIFAYGOTGSGKSYMMGY 121  
Db 72 AYDHCFSWDSVEKRYAGODIVFKCLGENIIONAFDGVNACIFAYGOTGSGKSYTMGCT 131  
Qy 122 GKEHGIVPRICODMERRINELQDKN--LTCTVEVSYLEIYNERVDDLNP-STKGNLKV 178  
Db 132 ADQPGILPRLCGSLFER---TQKEENEOSFKVEVSYMEIYNEKVDLLDPKGSROTLLKV 188  
Qy 179 REHPSTGPVEDLAKLVRSFOEINLMDGKNKARTVAATNNETSRSASHAVFTLLTQK 238  
Db 189 REHSVLGPVVDGSLKLAVTSYKDIESLMSGNKSRTVAATNNESRSASHAVFKITLTHT 248  
Qy 239 WHDETKMDTEKVAKISLVDLAGESEKATSTGATGARLKEGAEINRSLSTLGRVIALADM 298  
Db 249 LYDVKSCTSGEKGKSLVLDLAGESEKATSTGATGARLKEGAEINRSLSTLGRVIALADM 308  
Qy 299 SSGKOKKQNLVPRDSVLTWLKDSLGGNSMTAMIAISPADINEFTLSTLRVADSAC 357  
Db 309 SAGK-NKMKFVPRDSVLTWLKDSLGGNSKTMAMVATVSPADNVDETLSTLRVADRAK 366  
RESULT 29  
ADJ69671  
ID ADJ69671 standard; protein; 1826 AA.  
XX  
XX ADJ69671;  
AC  
XX  
XX 06-MAY-2004 (first entry)  
DT  
XX  
XX Human heat mitochondrial protein as a therapeutic target Segid1477.  
DE  
XX  
XX mitochondrial; human; screening assay; diabetes mellitus;  
KW Huntington's disease; osteoarthritis;  
KW Leber's hereditary optic neuropathy; LHON;  
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;

KM myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;  
 KM neuroprotective; neurotropic; antidiabetic; anticonvulsant; antiarthritic;  
 KM osteopathic; ophthalmological; cyrostatic.  
 OS Homo sapiens.  
 PN WO2003087768-A2.  
 XX 23-OCT-2003.  
 PD 04-APR-2003; 2003WO-US010870.  
 PF 12-APR-2002; 2002US-0372843P.  
 PR 17-JUN-2002; 2002US-0389987P.  
 PR 20-SEP-2002; 2002US-0412418P.  
 XX (MITO-) MITOKOR.  
 PA (BUCK-) BUCK INST AGE RES.  
 PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;  
 PI Warnock DE;  
 DR WPI; 2003-845369/78.  
 XX Identifying a mitochondrial target for drug screening assays and for  
 PT treating diseases associated with altered mitochondrial function.  
 PT comprises detecting a modified polypeptide in a sample and correlating  
 PT with the disease.  
 PS Claim 1; SEQ ID NO 1477; 180pp; English.  
 XX This invention relates to novel mitochondrial targets that can be used  
 CC for therapeutic intervention in treating a disease associated with  
 CC altered mitochondrial function. Specifically, it refers to a method for  
 CC identifying proteins of the human heart mitochondrial proteome that are  
 CC useful for drug screening assays, as well as therapeutic targets. The  
 CC present invention describes a method for identifying such proteins that  
 CC can be used in the treatment of various diseases associated with altered  
 CC mitochondrial function including diabetes mellitus, Huntington's disease,  
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial  
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy  
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these  
 CC compositions have neuroprotective, neurotropic, antidiabetic,  
 CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and  
 CC cyrostatic activities. This polypeptide sequence is a human heart  
 CC mitochondrial protein of the invention.  
 XX Sequence 1826 AA;  
 SQ  
 Query Match 55.4%; Score 1016.5; DB 7; Length 1826;  
 Best Local Similarity 58.5%; Pred. No. 2.7e-90;  
 Matches 210; Conservative 49; Mismatches 87; Indels 13; Gaps 6;  
 QY 3 GGGNKKVVRVPPNAREIDRGAACIVMEGNTLTTPPGAEEKARKSGKTIIMDPKAF 62  
 DB 2 GDSKVVAARIRPMNRREDLHTKCVVDANKVILNPVNTLSKGDARQ-----PKCF 56  
 QY 63 AFDRSYWSFDKNA-PNYARQEDLFQDLGVPLLDNAFGYNNCIPAYGQTSGSGSYMMGY 121  
 DB 57 AYDHCWMSMDESVKEXYAGQDIYFKCIGENIILNARDGVNACIFAYGQTSGSGSYMMGY 116  
 QY 122 GKEHGVIPRIICQMFRINELQDKN--LTCYVEVYLEYNRRVVDLNP-STKGNLKY 178  
 DB 117 ADPPGLIPRLCSGLFER---TQKEENBOSFKVEVSIMEYNEKVDLDLPKSGRQTLKY 173  
 QY 179 REHPSTGPYVEDLAKIVVRSFOEINLMDGNKARTVAATNNMETSRSRAVETLTITJOK 238  
 DB 174 REHSVAGPYVDGSLKLAATSYKQIESLSMGSKSRVAAATNMEESSRSRAVAKITLITR 233  
 QY 239 WHDEETKMDTEKYAKISLVDLAGESEATSTGATGARLKEGAEINRSLSTIGRAVIALADM 298  
 DB 234 LYDAKSGTSGEKVKLSLVDLAGESEATSTGATGARLKEGAEINRSLSTIGRAVIALADM 293

QY 299 SSGKOKNOLVPRDSVLTWLLKDSLGNSMTAMIAISPADINFEETLSTURYADSAK 357  
 DB 294 SAGK-NKMKFVPIRDSVLTWLLKDSLGNSKTMVAIVSPADNVDETLSTURYADRAK 351  
 RESULT 30  
 ID ADL83235  
 ADL83235 standard; protein; 1826 AA.  
 XX ADL83235;  
 AC ADL83235;  
 DT 17-JUN-2004 (first entry)  
 XX 17-JUN-2004 (first entry)  
 DE Human PRO60891, SEQ ID 437.  
 XX Immunosuppressive; Cyrostatic; Arthritic; Antirheumatic; Antianemic;  
 KM Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory;  
 KM Gene Therapy; PRO; B cell related disorder; cancer;  
 KM Immune-mediated inflammatory disease; human.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 PN WO2004024097-A2.  
 XX 25-MAR-2004.  
 PD 15-SEP-2003; 2003WO-US029097.  
 PR 16-SEP-2002; 2002US-0411392P.  
 XX (GETH ) GENENTECH INC.  
 PA Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;  
 PI Wu TD;  
 DR WPI; 2004-329389/30.  
 DR N-PSDB; ADL83234.  
 XX New PRO polypeptide, useful for diagnosing and treating a B cell related  
 PT disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune  
 PT mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.  
 XX Claim 10; Fig 437; 695pp; English.  
 PS The present invention relates to PRO proteins and their coding sequences.  
 CC The PRO proteins are useful for diagnosing and treating a B cell related  
 CC disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide  
 CC antigen unresponsiveness, selective IGA deficiency, selective IGM  
 CC deficiency, selective deficiency of IGA subclasses, immunodeficiency with  
 CC hyper IGM, transient hypogammaglobulinemia of infancy, Burkitt's  
 CC lymphoma, intermediate lymphoma, follicular lymphoma, type II  
 CC anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or  
 CC ankylosing spondylitis. The PRO proteins are also useful for preparing a  
 CC medicament for treating a condition that is responsive to the PRO  
 CC protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO  
 CC coding sequences are useful as hybridization probes in chromosome and  
 CC gene mapping, in preparing PRO proteins, or in generating transgenic  
 CC animals or knockout animals, which in turn are useful in the development  
 CC and screening of therapeutically useful reagents.  
 XX Sequence 1826 AA;  
 SQ  
 Query Match 55.4%; Score 1016.5; DB 8; Length 1826;  
 Best Local Similarity 58.5%; Pred. No. 2.7e-90;  
 Matches 210; Conservative 49; Mismatches 87; Indels 13; Gaps 6;  
 QY 3 GGGNKKVVRVPPNAREIDRGAACIVMEGNTLTTPPGAEEKARKSGKTIIMDPKAF 62  
 DB 2 GDSKVVAARIRPMNRREDLHTKCVVDANKVILNPVNTLSKGDARQ-----PKCF 56  
 QY 63 AFDRSYWSFDKNA-PNYARQEDLFQDLGVPLLDNAFGYNNCIPAYGQTSGSGSYMMGY 121

Db 57 AYDHCFWMSDESVEKXYAGDIIVFKCLGENILQNAFDGVNACIFAYGQTGSGKSYTMGT 116  
Qy 122 GKEHGVIPRI CODMFRINELQDKN--LTCTVEVSYLEIYNERVDLNP-STKGNLKY 178  
Db 117 ADQPGIIPRLCSGLFER--TQKEENBEO\$FKVEVSymeIYNEKVRDLDPKGSROTlKY 173  
Qy 179 REHPSGTPIVEDLAKLVNRSFOEIEIENLMDGNCARTVAATNMNETSSRSHAVFTLTlTQK 238  
Db 174 REHSVULGPYVDGLSKLAATSYKDIESIM\$EGNKSRTVAATNMNEBSSRSHAVLKITlTHT 233  
Qy 239 WHDEETKMDTEKYAKISLYVDLAGSERATSTGATGARLKEGAEINRSISTLGRVIAALADW 298  
Db 234 LYDAKSGTSGEKYKXLSLYVDLAGSERATKTGAAGDRLKEG\$NINESITTLGLVISALADQ 293  
Qy 299 SSGKQKKNQLVPRDSVLTWLLKDSLGNSMTMIAAISPADINFEETLSTLRVADS\$K 357  
Db 294 SAGK-NKNKFVVPYRDSVLTWLLKDSLGNSKTMVATVSPADNYDETlSTLRVADRAK 351

Search completed: September 5, 2006, 18:04:43  
Job time : 201 secs